



MATCH WITH FIG. 1A

241	AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG	300
	-----+-----+-----+-----+-----+-----+-----+	
	TTCGATAAGAGAAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC	
	K L F S F T K Y F L K I E K N G K V S G	
301	ACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT	360
	-----+-----+-----+-----+-----+-----+-----+	
	TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA	
	T K K E N C P Y S I L E I T S V E I G V	
361	GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAACTC	420
	-----+-----+-----+-----+-----+-----+-----+	
	CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG	
	V A V K A I N S N Y Y L A M N K K G K L	
421	TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA	480
	-----+-----+-----+-----+-----+-----+-----+	
	ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT	
	Y G S K E F N N D C K L K E R I E E N G	

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

481	TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG	540
	-----+-----+-----+-----+-----+-----+	
	ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC	
	Y N T Y A S F N W Q H N G R Q M Y V A L	
541	AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC	600
	-----+-----+-----+-----+-----+-----+	
	TTACCTTTTCCTCGAGGTTCTCTCCTGTCTTTTGTGCTTCCTTTTGTGGAGACGAGTG	
	N G K G A P R R G Q K T R R K N T S A H	
601	TTTCTTCCAATGGTGGTACACTCATAG	627
	-----+-----+-----	
	AAAGAAGGTTACCACCATGTGAGTATC	
	F L P M V V H S *	

FIG.1C

	1		50
FGF4	MS.GPGTAAV ALLPAVLLAL LA.....	.PWAGRGGAA APTAPNGTLE	
FGF6	MSRGAGRLQG TLWALVFLGI LV.....	.GMVVPSPAG TR.ANNTLLD	
FGF5	.....MSL SFLLLLFFSH LILSAWAHGE	KRLAPKGQPG PAATDRNPIG	
FGF1	.....	.....	
FGF2	.....	.....	
FGF9	.....	..MAPLGEVG NYFGVQDAVP	
FGF7	.....MHKW ILTWILPTLL .....	YRSCF HIICLVGTIS	
KGF2	.....MWKW ILTHCASAFP HLPGCCCCCF	LLLFLVSSVP	
FGF3	.....	.....MGL IWLLLLSLLE	
FGF8	MGSPRSALSC LLLHLLVLCL QAQVRSAAQK	RGPGAGNPAD TLGQGHEDRP	

	51		100
FGF4	AELERRWESL VALSLARLPV AA..QPKEAA	VQSGAGDY.. ...LLGIKRL	
FGF6	S...RGWGTL LSRSRAGLAG EI.....AG	VNWESG.Y.. ...LVGIKRQ	
FGF5	SSSRQSSSSA MSSSSASSSP AASLGSQGSG	LEQSSFQW.. ...SPSGRRT	
FGF1	.....MAEG EITTF TALTE KFN...LPPG	.....N.. ...YK...KP	
FGF2	.....MAAG SITTLPALPE DGGSGAFPPG	.....H.. ...FK...DP	
FGF9	FGNVPVLPVD SPVLLSDHLG QSEAGGLPRG	PAVTDLDH.. ...LKGILRR	
FGF7	LACNDMTPEQ M...ATNVNC .....	SSPE RHTRSYDY.. ...MEGGDIR	
KGF2	VTCQALGQDM VSPEATNSSS SSFSSPSSAG	RHVRSYNH.. ...LQ.GDVR	
FGF3	PGWPAAGPGA .....	...RLRRDAG GRGGVYEH.. ...L.GGAPR	
FGF8	FGQRSRAGKN FTNPAPNYPE EGSKEQRDSV	LPKVTQRHVR EQSLVTDQLS	

MATCH WITH FIG. 2B

FIG. 2A



MATCH WITH FIG. 2B

	201		250
FGF4	.....	GM.....FI ALSKNGKTKK G..NRVSPTM	KVTHFLPRL.
FGF6	.....	GT.....YI ALSKYGRVKR G..SKVSPIM	TVTHFLPRI.
FGF5	.....	TEKTGREWYV ALNKRKGAKR GCSPRVKPQH	ISTHFLPRFK
FGF1	.....	...AEKNWFV GLKKNNGSCKR G..PRTHYGQ	KAILFLPLPV
FGF2	.....	...T..SWYV ALKRTGQYKL G..SKTGPGQ	KAILFLPMSA
FGF9	HV.....	..DTGRRYYV ALNKDGTPRE G..TRTKRHQ	KFTHFLPRPV
FGF7	.....	AKW THNGGEM.FV ALNQKGIPVR G..KKTKKEQ	KTAHFLPMAI
KGF2	.....	FNW QHNGRQM.YV ALNGKGAPRR G..QKTRRKN	TSAHFLPMVV
FGF3	TVSSTPGARR	QPSAERLWYV SVNGKGRPRR G..FKTRRTQ	KSSLFLPRVL
FGF8	.....	.....EGWYM AFTRKGRPRK G..SKTRQHQ	REVHFMKRLP

	251		300
FGF4	.....	.....	.....
FGF6	.....	.....	.....
FGF5	QSEQPELSFT	VTVPEKKNPP SPIKSKIPLS APRKNTNSVK	YRLKFRFG..
FGF1	SSD.....	.....	.....
FGF2	KS.....	.....	.....
FGF9	DPDKVPELYK	DILSQS....	.....
FGF7	T.....	.....	.....
KGF2	HS.....	.....	.....
FGF3	DHRDHEMVRQ	LQSGLP RPPG KGVQPRRRRQ KQSPDNLEPS	HVQASRLGSQ
FGF8	RGHHTTEQSL	RFEFLNYPPF TRSLRGSQRT WAPEPR....	.....

MATCH WITH FIG. 2D

FIG. 2C

MATCH WITH FIG. 2C

301

FGF4	.....
FGF6	.....
FGF5	.....
FGF1	.....
FGF2	.....
FGF9	.....
FGF7	.....
KGF2	.....
FGF3	LEASAH
FGF8	.....

FIG.2D

GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA	60
CAACTCCAAA GGGATATACT TGTAAGAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA	120
CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC	180
CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTTTGGCA TCTAACATGG	240
TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA	300
CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA	360
CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG	420
CTTTTCCGAG GAGTTATGGA TGTTGGTGCA TTCACCTCTG GCCAGATCCG CGCCCAGAGG	480
GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT	540
CCAGTATGTT CCTTCTGATG AGACAATTC CAGTGCCGAG AGTTTCAGTA CA ATG	595
Met	
TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC	643
Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro	
GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC	691
Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val	
CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC	739
Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala	
ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG	787
Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg	
CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG	835
His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys	
CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG	883
Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys	
GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA	931
Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile	
ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC	979
Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn	
TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA	1027
Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu	
TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC	1075
Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr	

FIG.3A



AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT	1123
Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr	
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA	1171
Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg	
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG	1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC	1336
TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT	1396
AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT	1456
ATTCCAAGT GAAAAACATT GTGGCTGGT TTTTGTGTG TGTGTCAAG TTTTGTITT	1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG	1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT	1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTA CTGGAAA GCACTTGGGT CATATCATAT	1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA	1756
TAAACATGTT AGTGTGAAAC TGTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC	1816
TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT	1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG	1936
CACACCACAT GCATGTTTAC GACAAAGTGT TTTTAAAACT TGGCGAACAC TTCAAAAATA	1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA	2056
CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG	2116
AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT	2296
TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416

FIG. 3B

CCCAGGGGCT TAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAACCAA ATAAACTTG TTTTCTGTAA	2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTAATAAGT TTAACCTTTG GAAATGCTGG CGTTCTGTGA	2896
TTCTCCAACA AACTTATTTG TGCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT	2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTCCC	3016
ATTCTTCAA AAAACTGTAT TTCAGAAGAA ACACATTGA GGCAGTGTCT TTTGGCTTAT	3076
AGTTTAAATT GCATTTATC ATACTTTGCT TCCAATTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTTGTG GTTGGATCT GGATGTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAAGTAGGTA TCTTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT	3376
TATTTACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCTGTCT CTCCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TGCCTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT	3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA	4036

FIG.3C

ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAGA AAAAAAAG CAGTTCAGC	4096
CCTGAATGTT GTAGATTGA AAAAAAAAAA AAAAAAATC GAGGGGGGGC CCGTACCCAA	4156
TTCGCCCTAT AGTGAGTCGT A	4177

FIG.3D

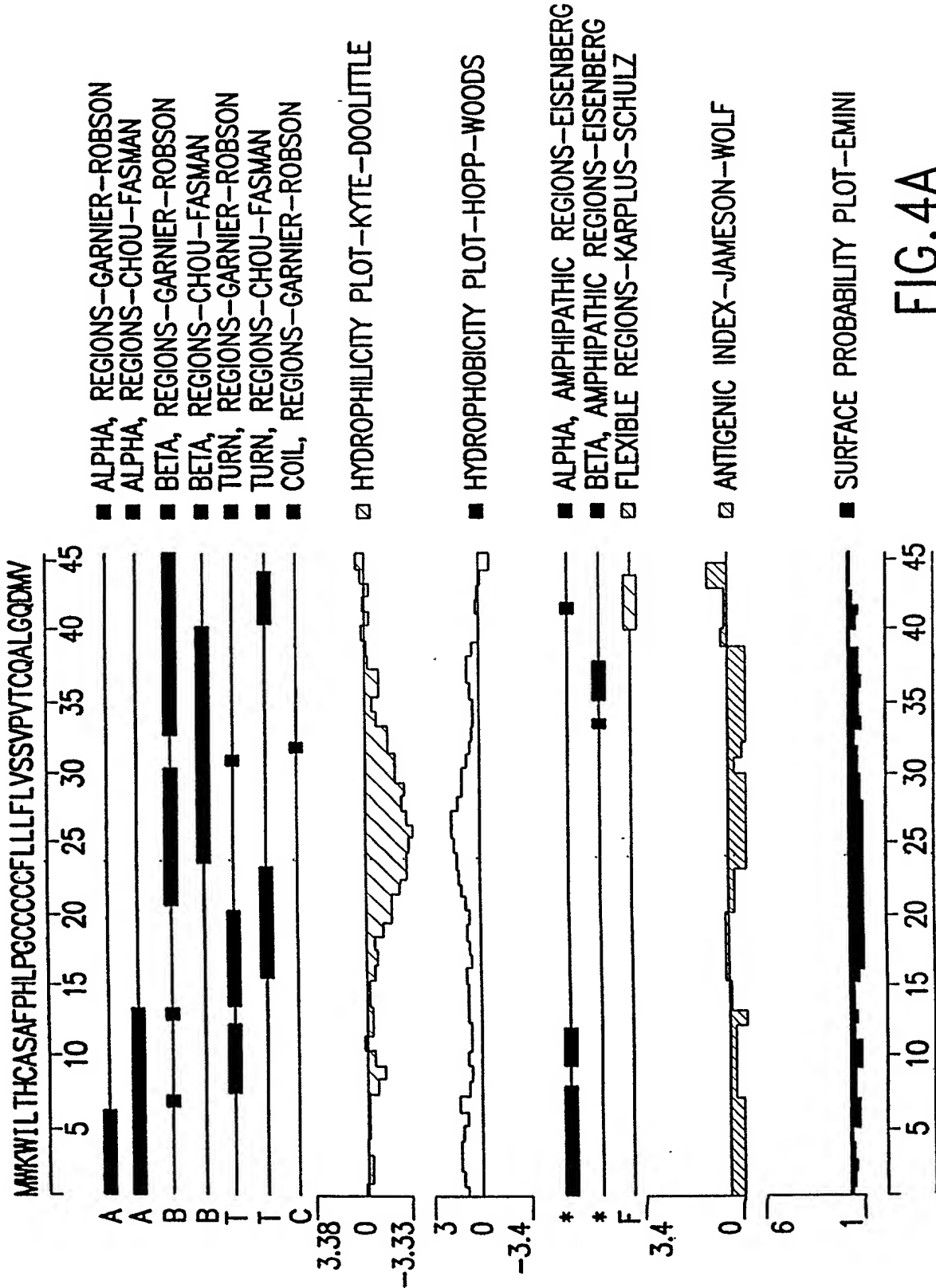
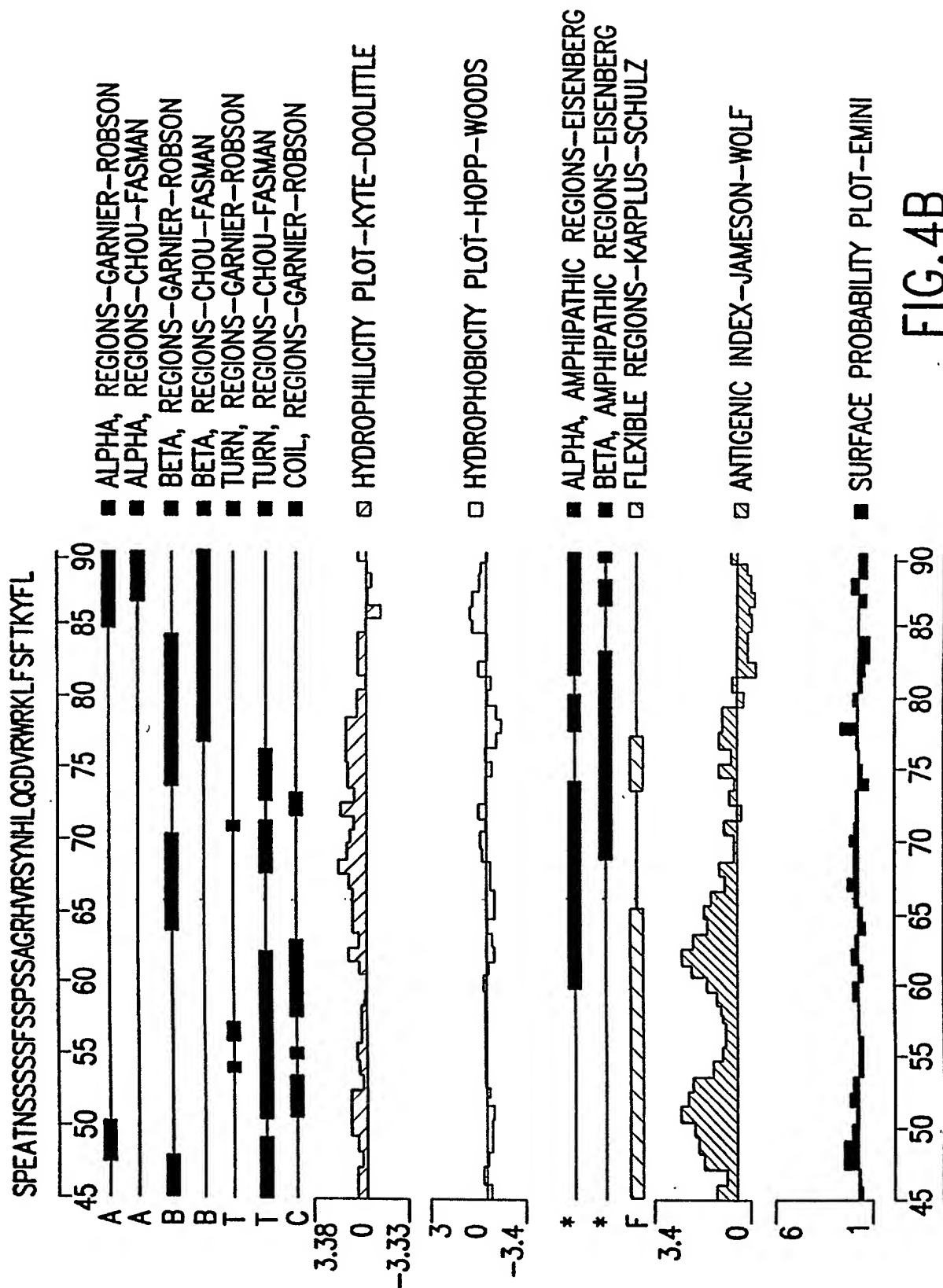
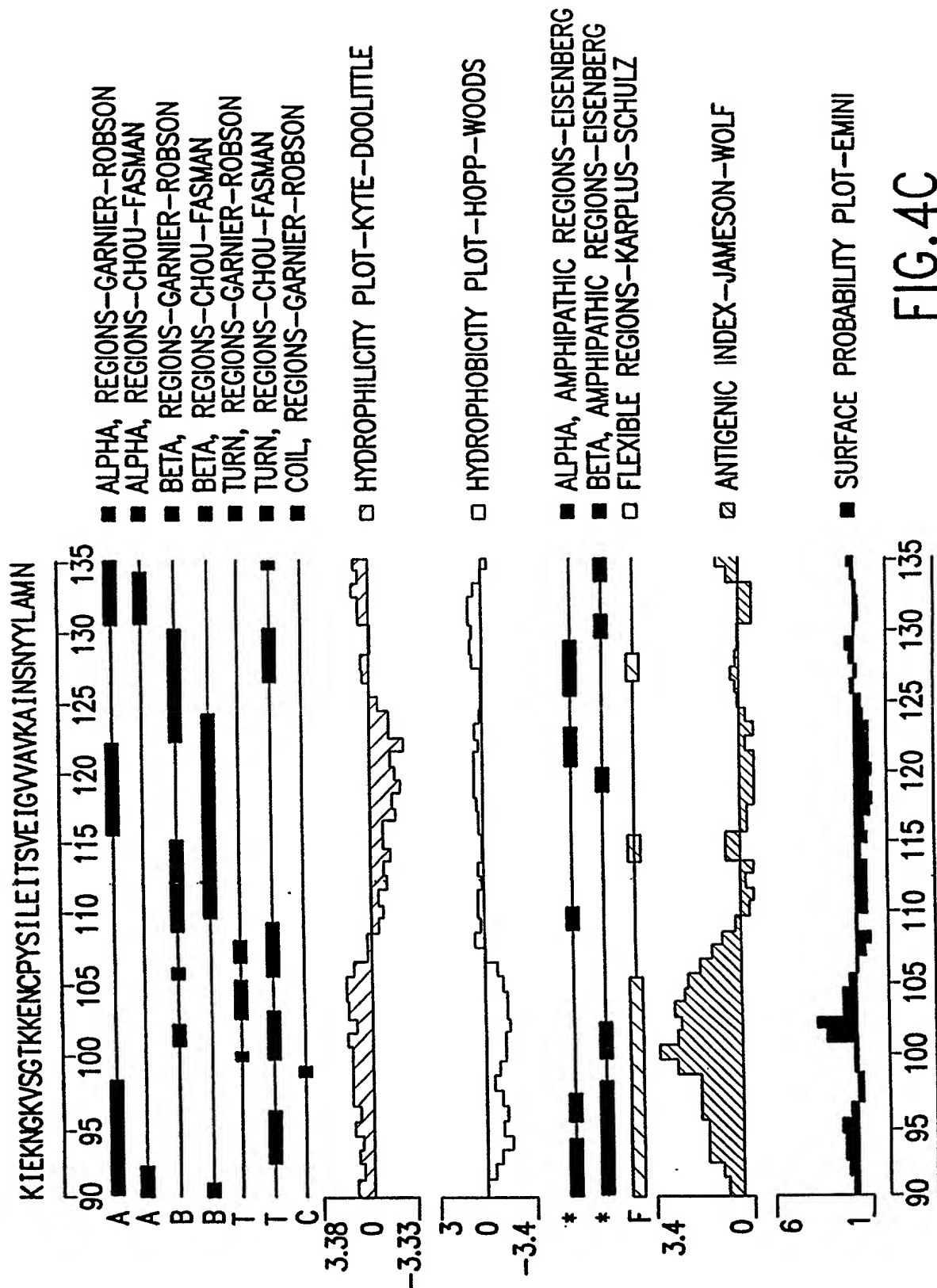


FIG. 4A





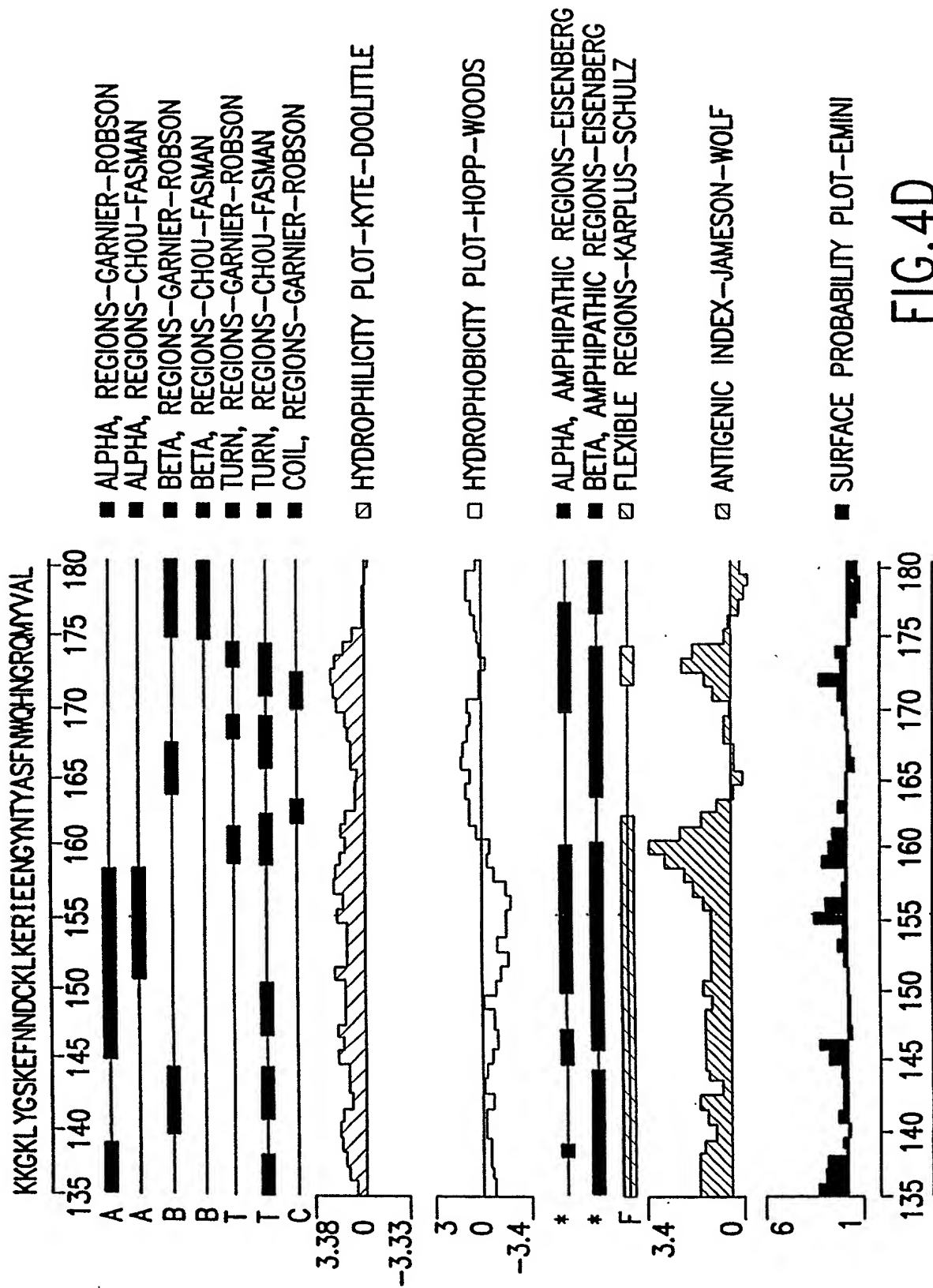
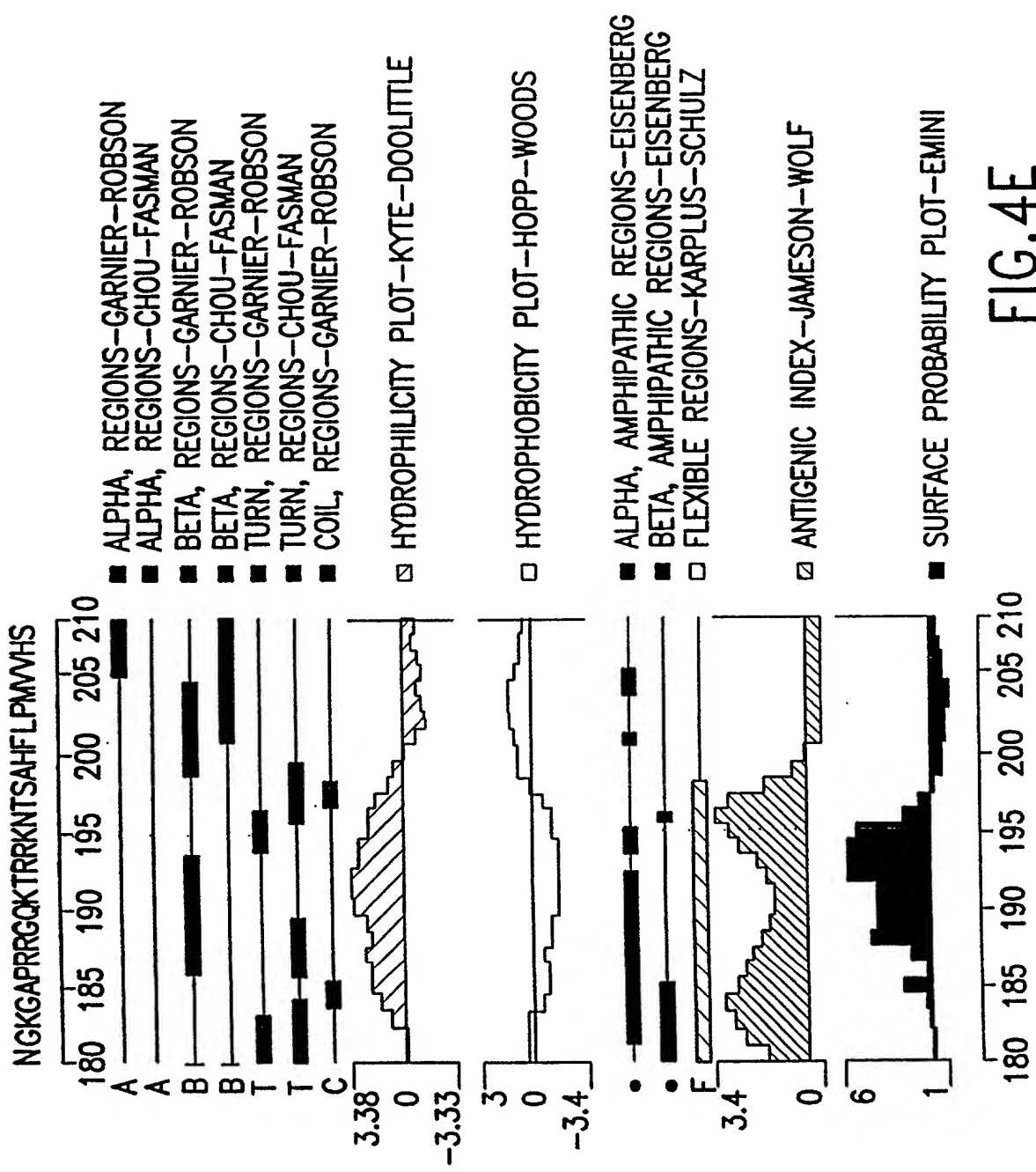


FIG.4D





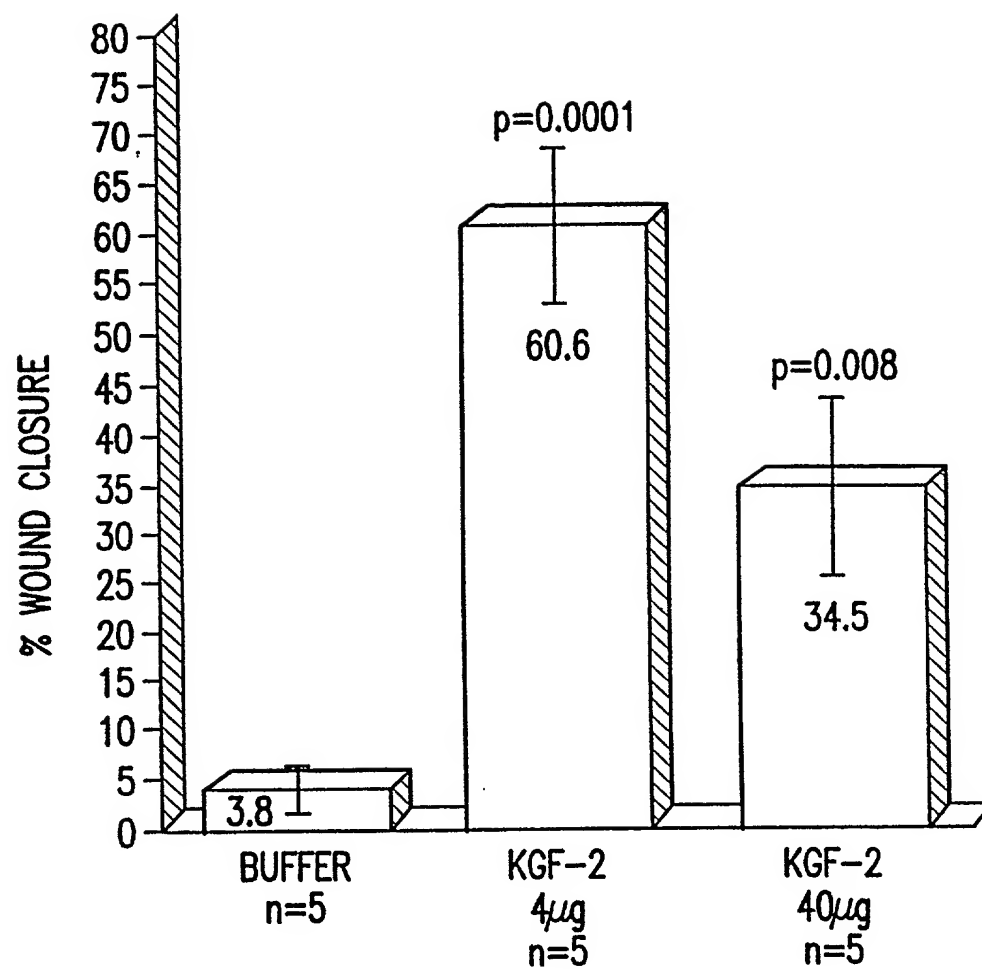


FIG.5

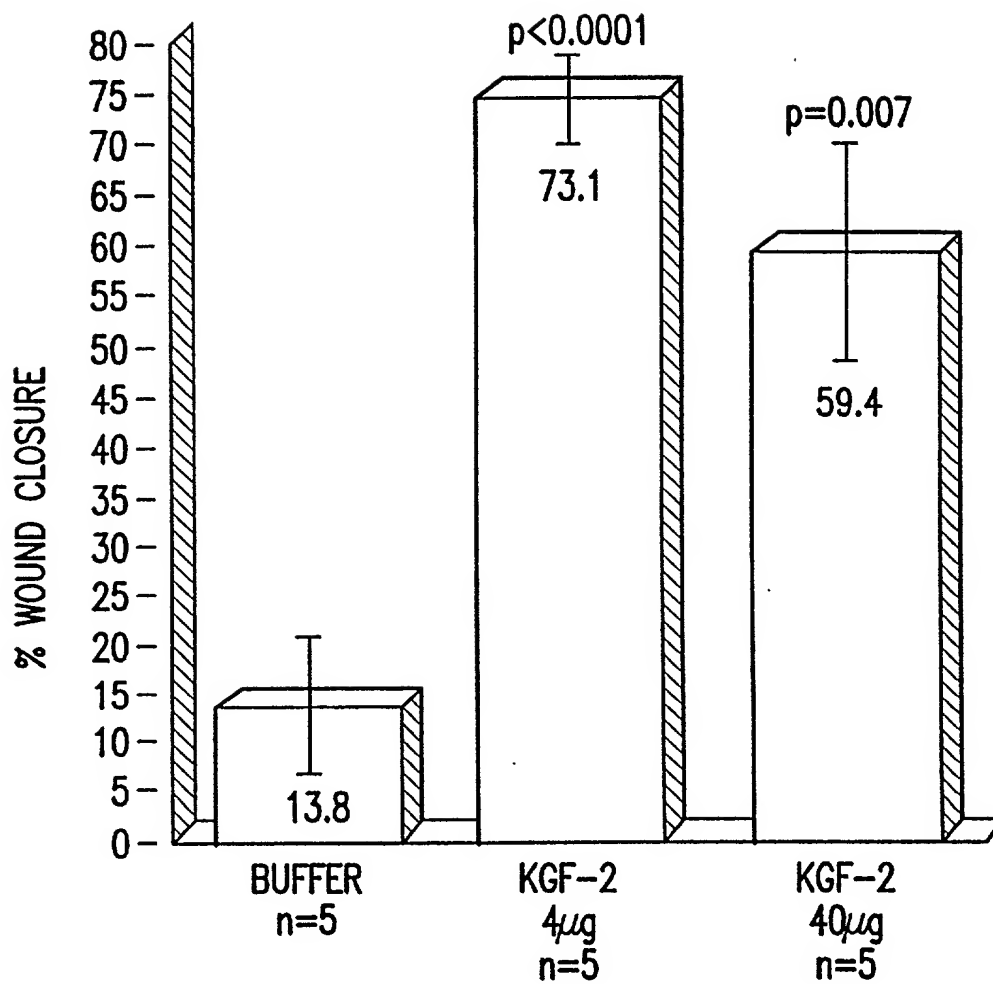


FIG.6

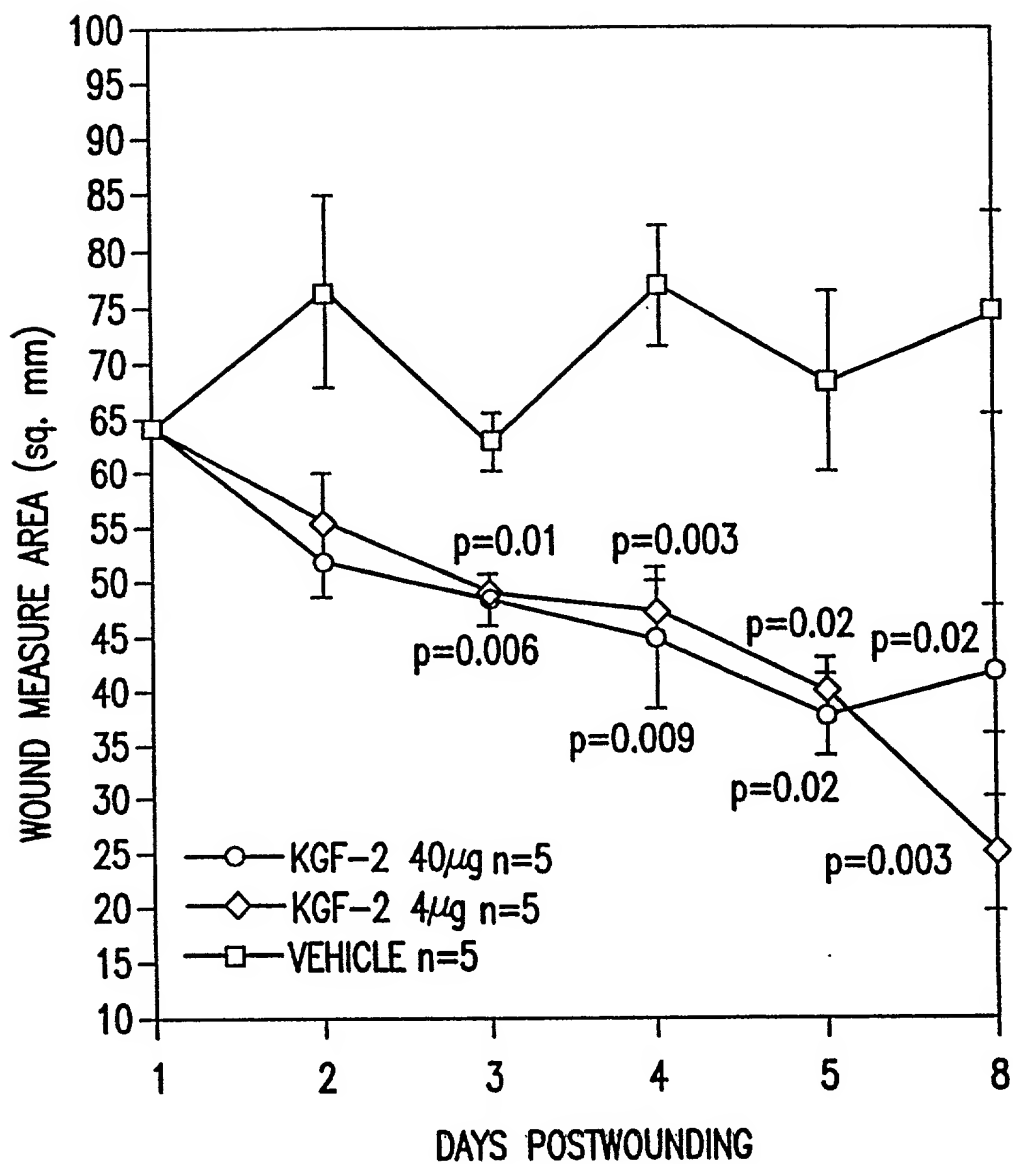


FIG.7

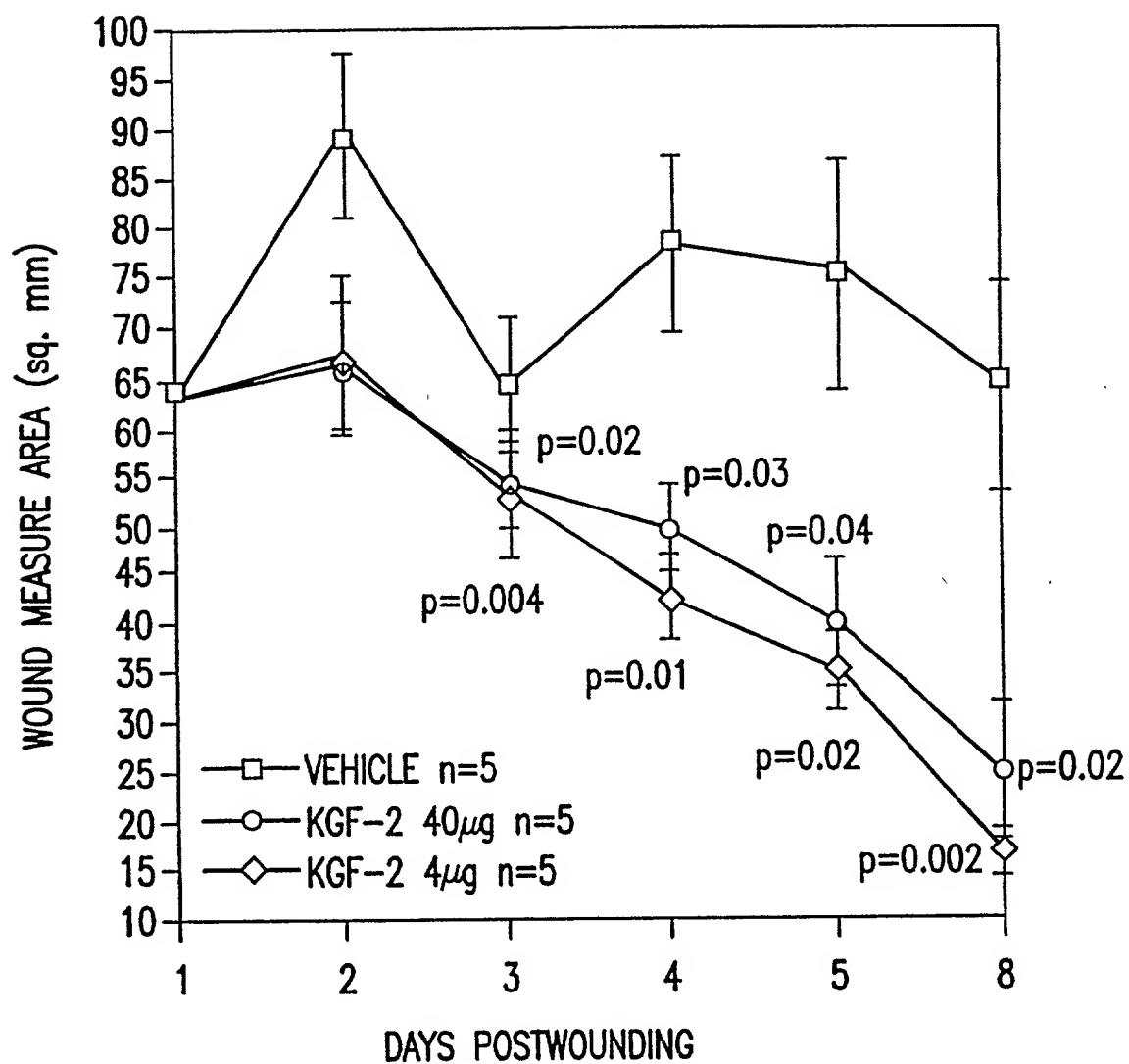
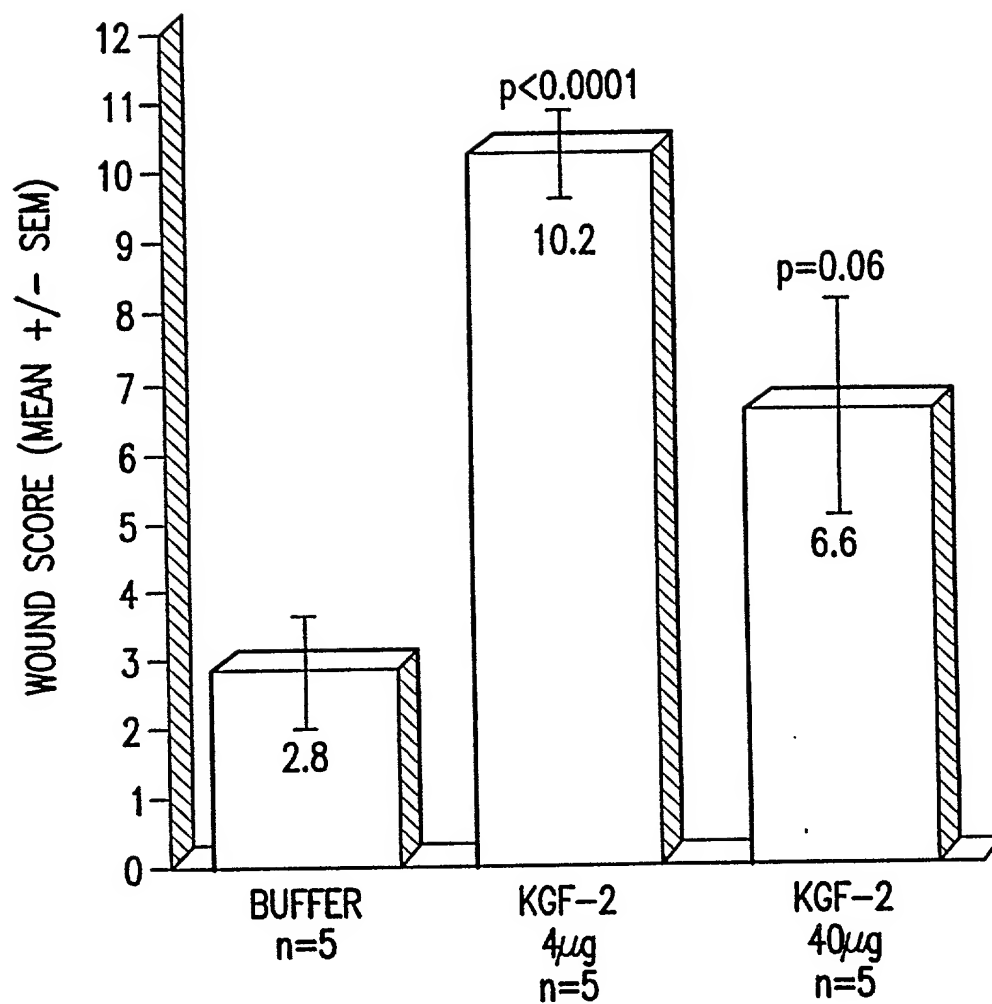
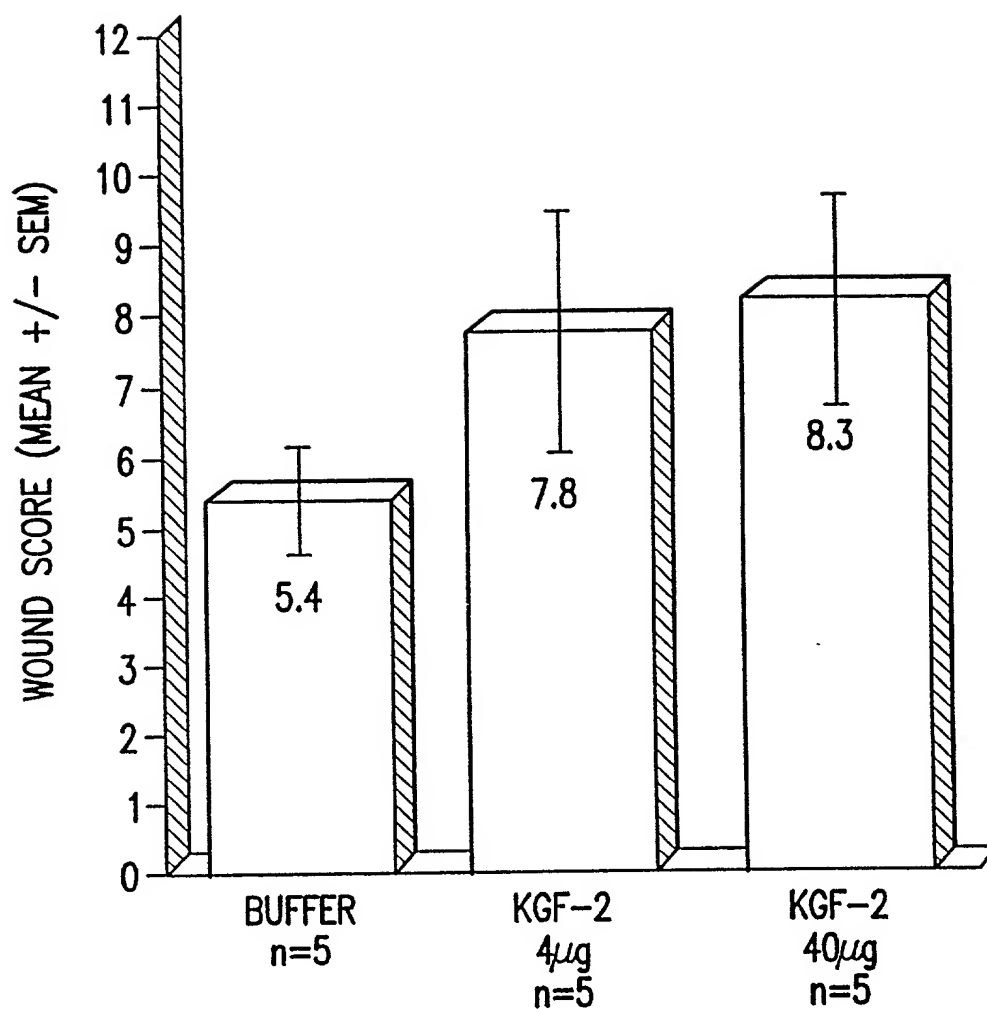


FIG.8



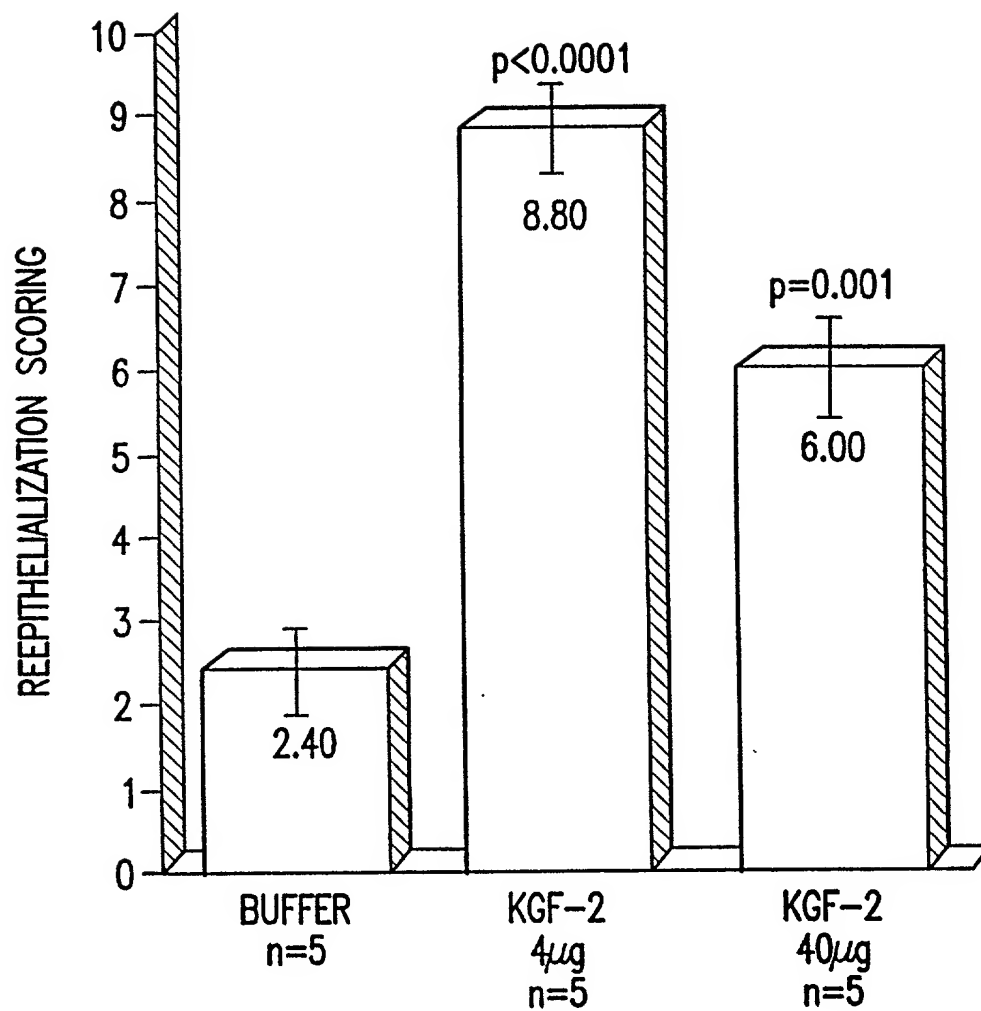
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
 4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
 10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
 4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
 7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM  
 10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10



ANTI-CYTOKERATIN IMMUNOSTAINING  
0-NO CLOSURE  
5-SLIGHT TO MODERATE CLOSURE  
10-COMPLETE CLOSURE

FIG.11

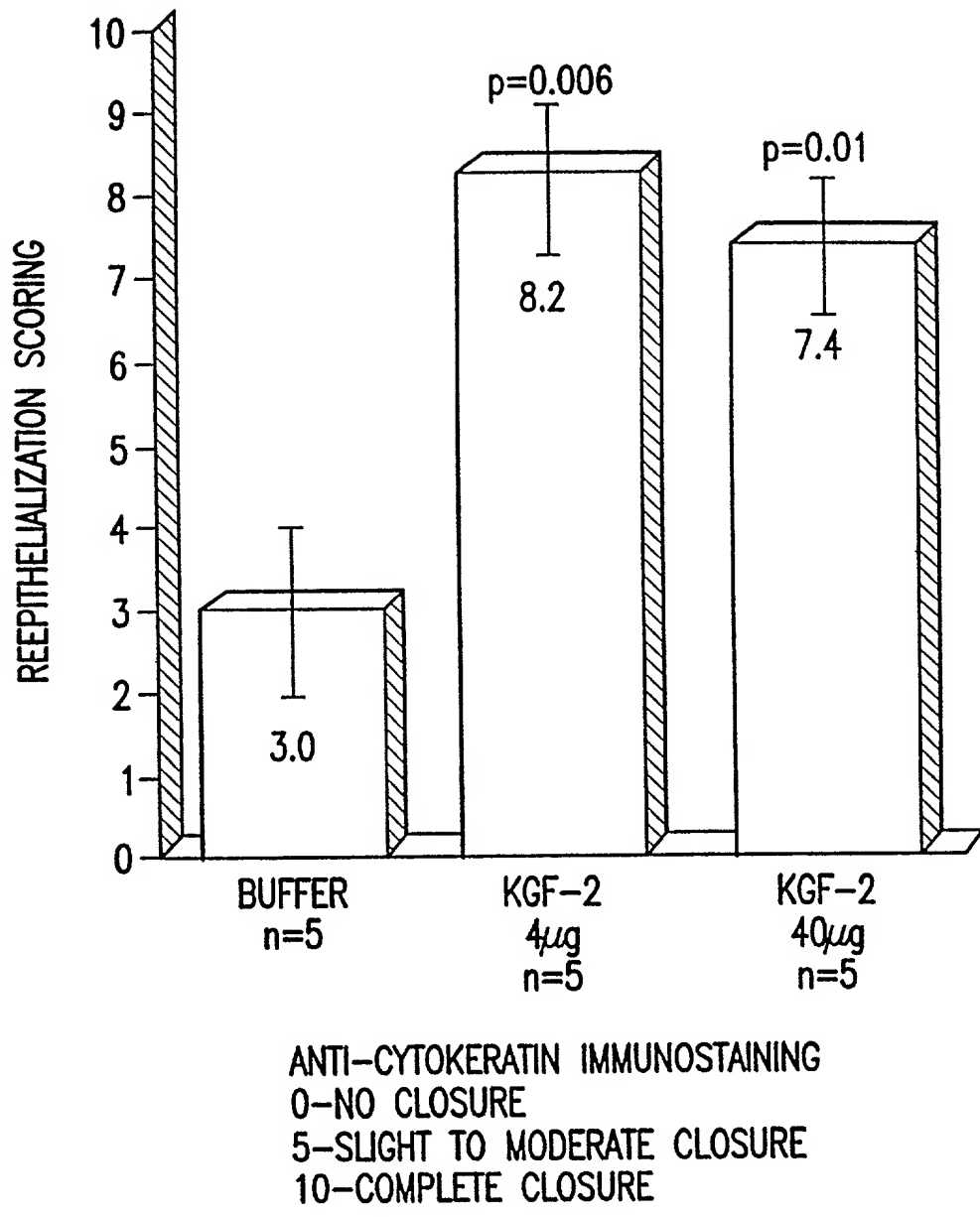
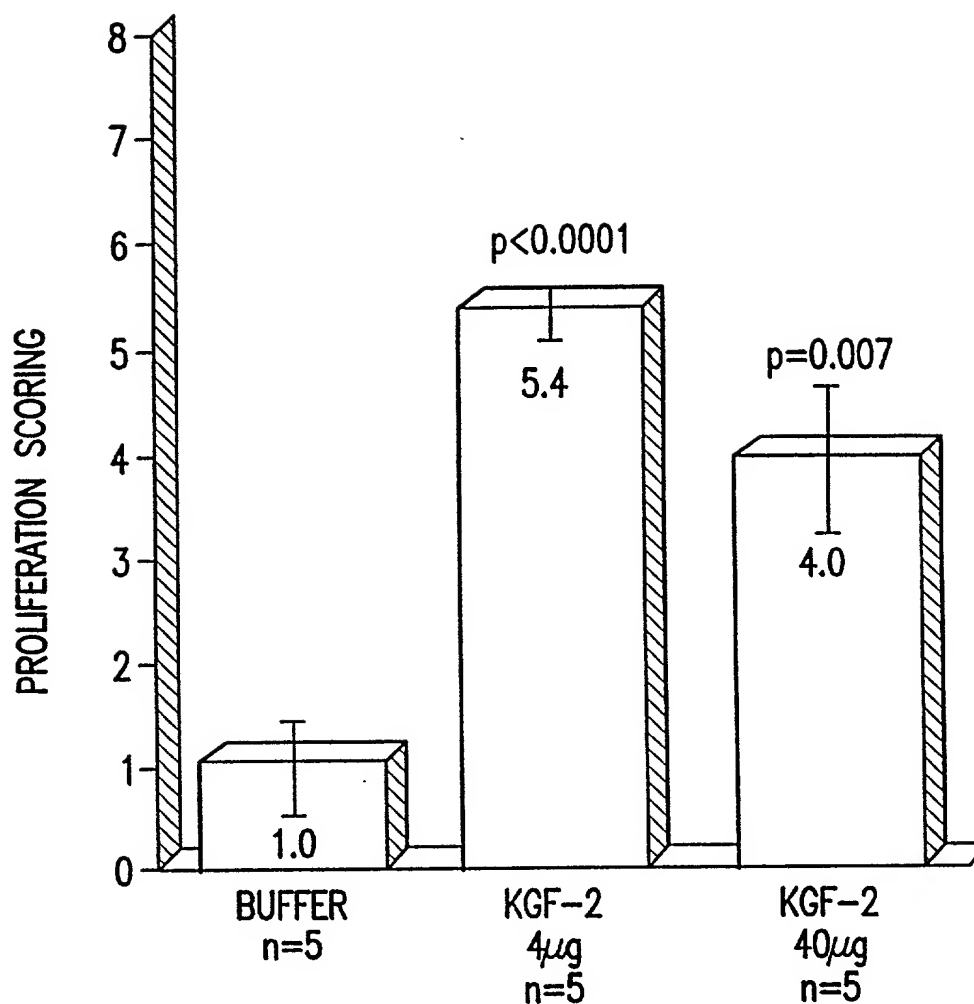


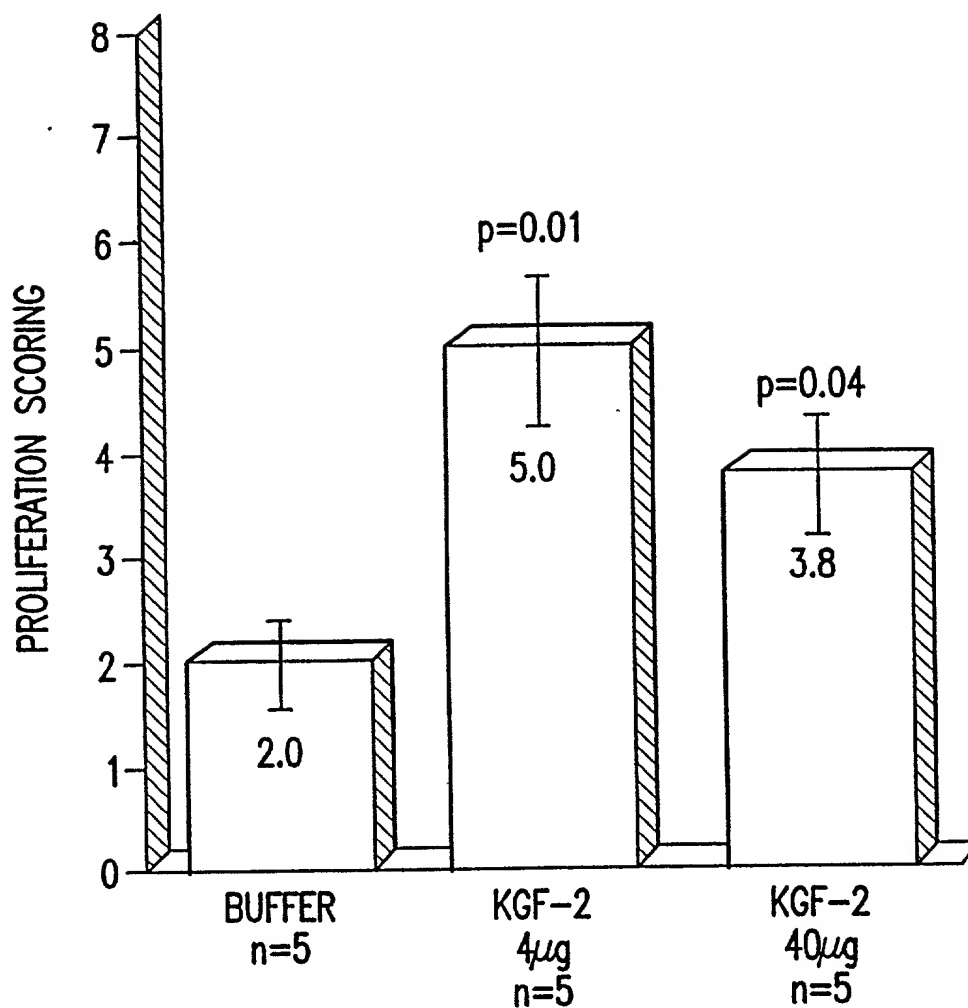
FIG.12





PCNA SCORING  
 0-2 SLIGHT PROLIFERATION  
 3-5 MODERATE PROLIFERATION  
 6-8 INTENSE PROLIFERATION

FIG.13



PCNA SCORING  
 0-2 SLIGHT PROLIFERATION  
 3-5 MODERATE PROLIFERATION  
 6-8 INTENSE PROLIFERATION

FIG.14

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC  
 AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCC  
 CGTCTTCOGCTGGTCGTCACGTTGTTCTTACAACCACCTGCAGGGTGACGTTG  
 GTTGGCGTAAACTGTTCTCTTTACCAAATACTTCCTGAAAATCGAAAAA  
 AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTG  
 GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG  
 CAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAG  
 AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT  
 ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT  
 GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG  
 GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD  
 VRWRKLFSTKYFLKIEKNGKVSGETTKENCPYSILEITSVEIGVVAVKAINSN  
 YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA  
 LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

kgf-2 synthetic cys37 Bam HI  
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

FIG.15

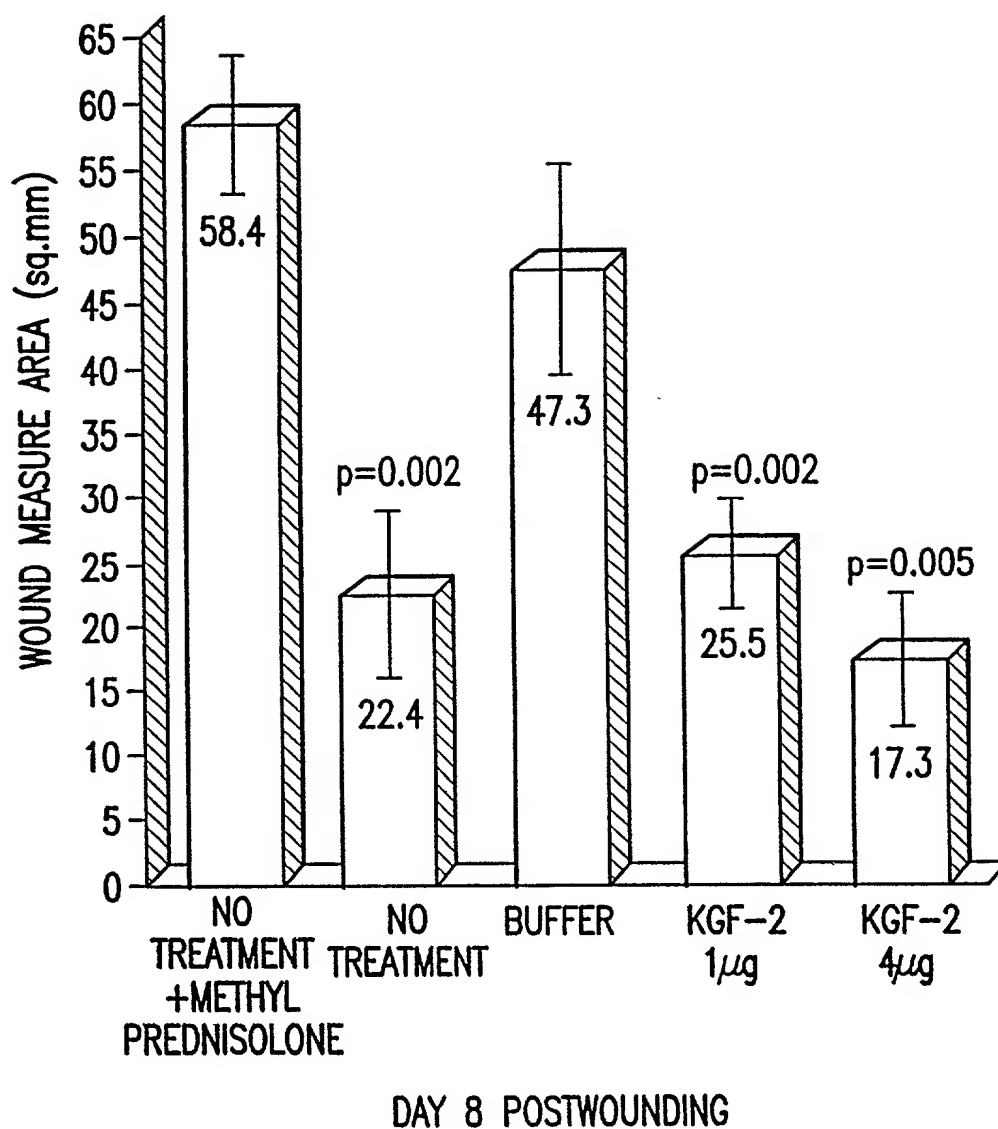
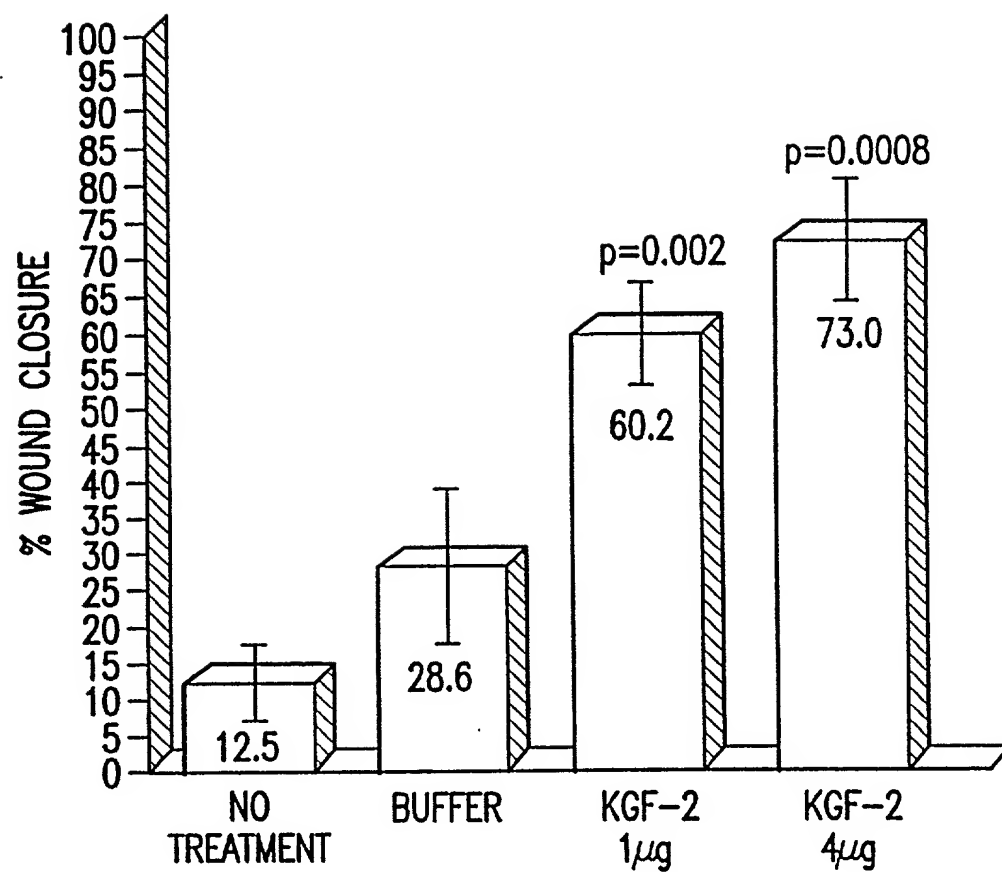


FIG.16



GLUCOCORTICOID TREATED ANIMALS

FIG.17

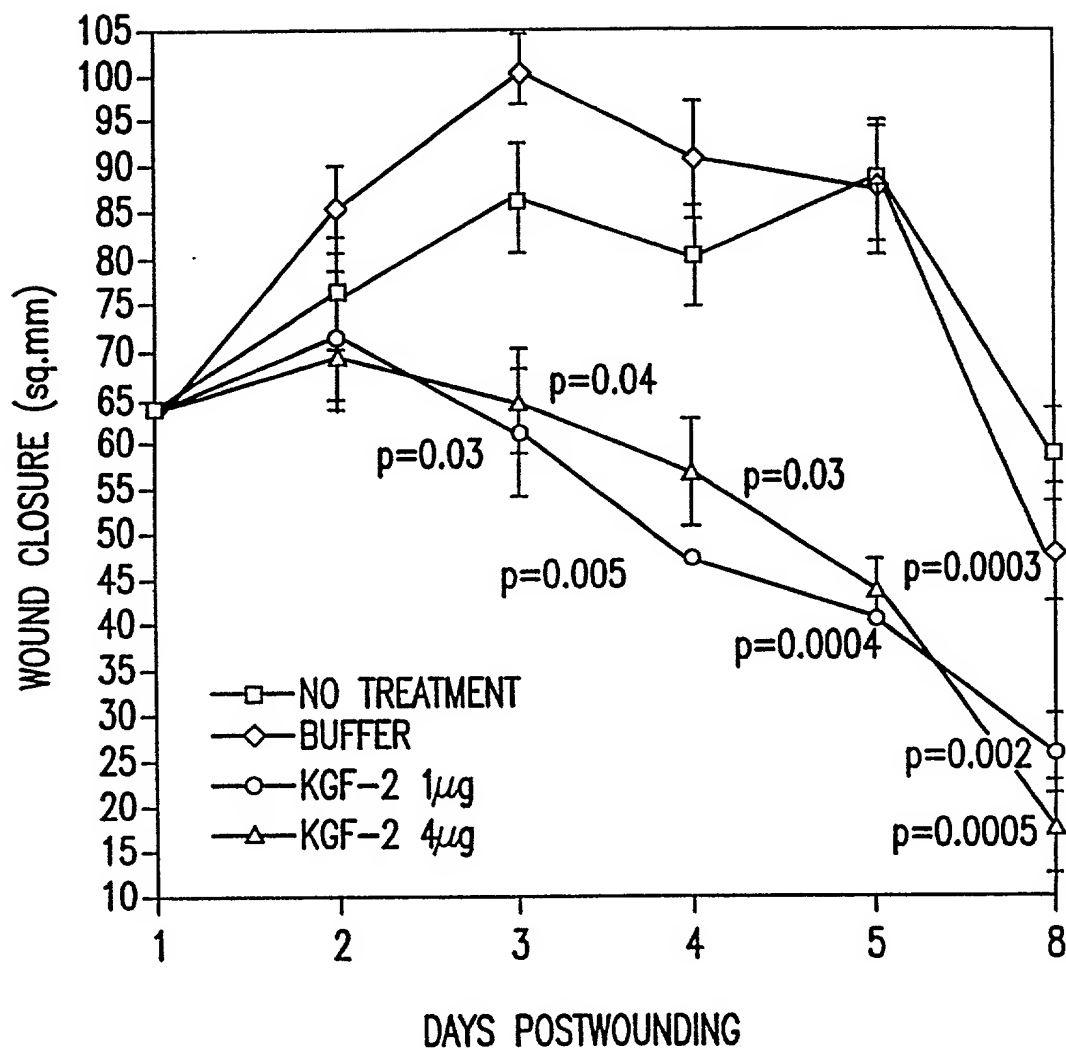


FIG.18

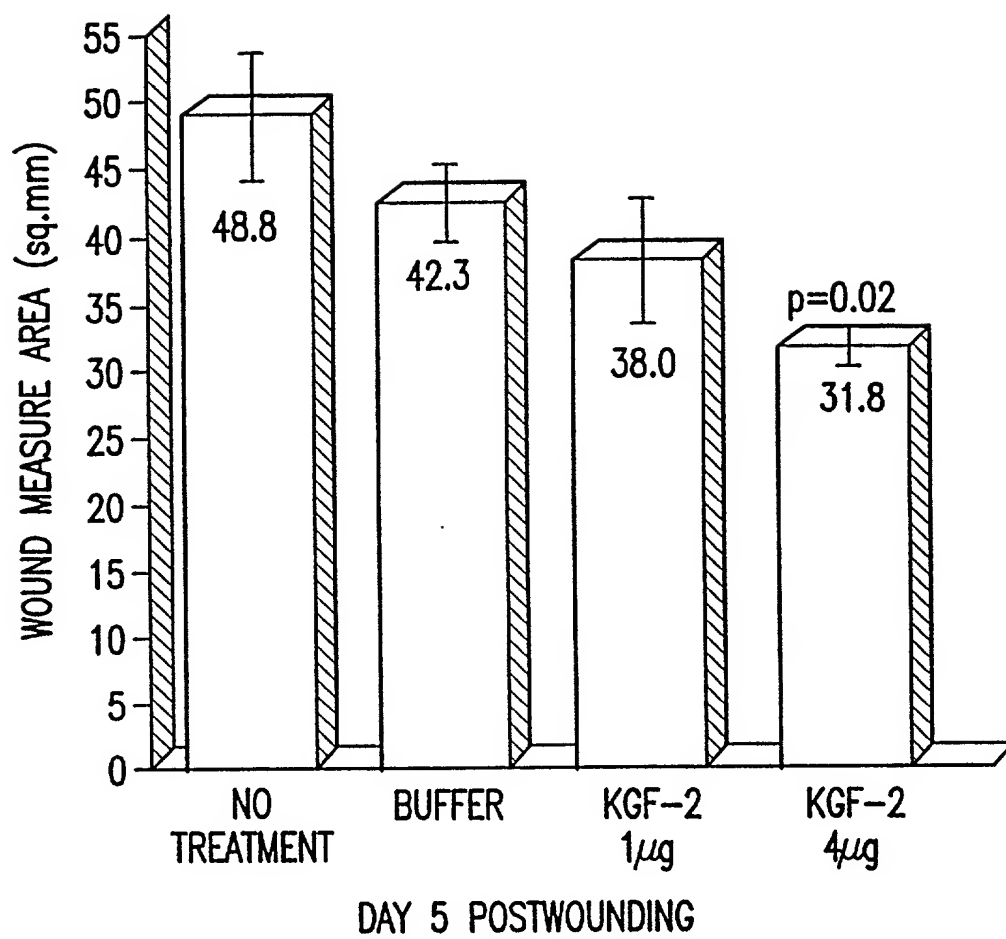
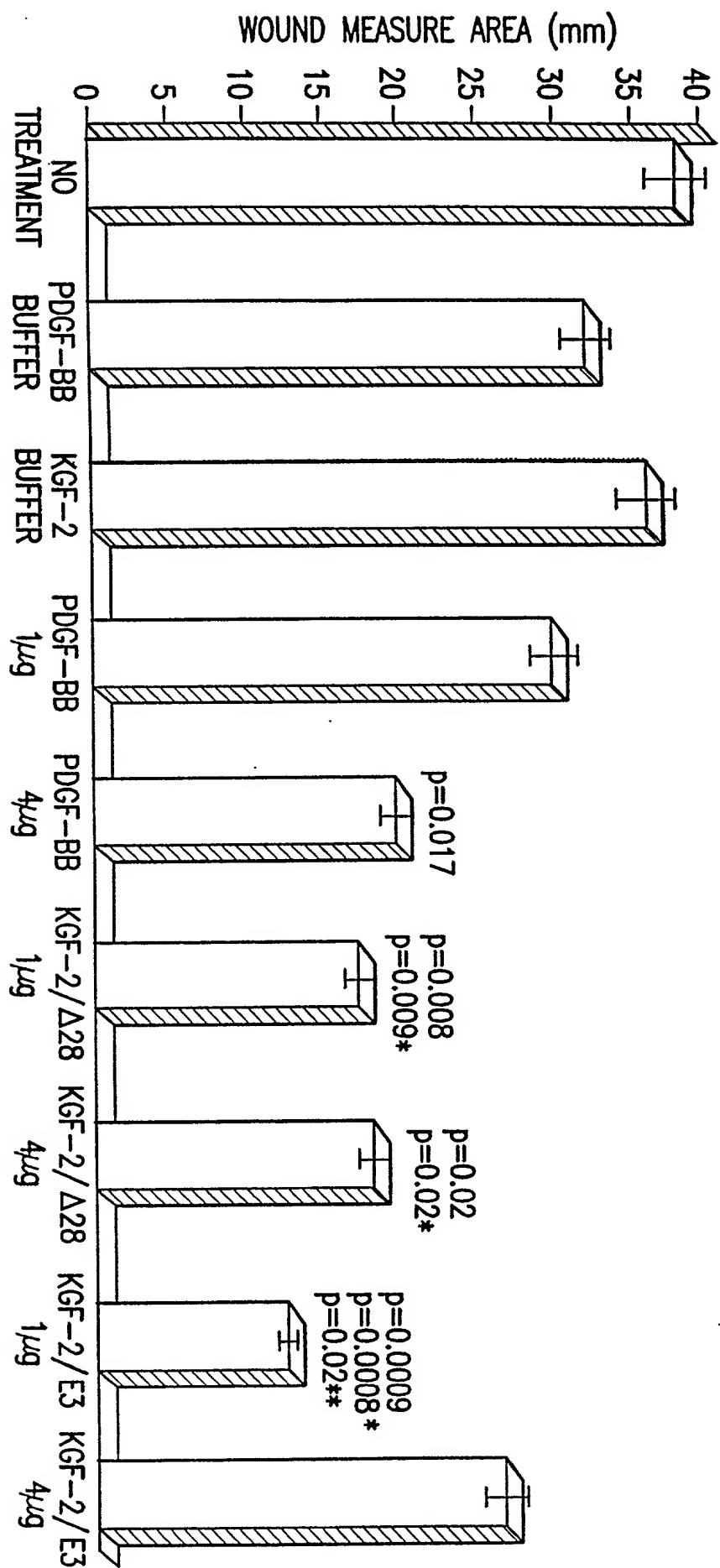


FIG.19A



DAY 10 POSTWOUNDING

FIG.19B

100345242 010402



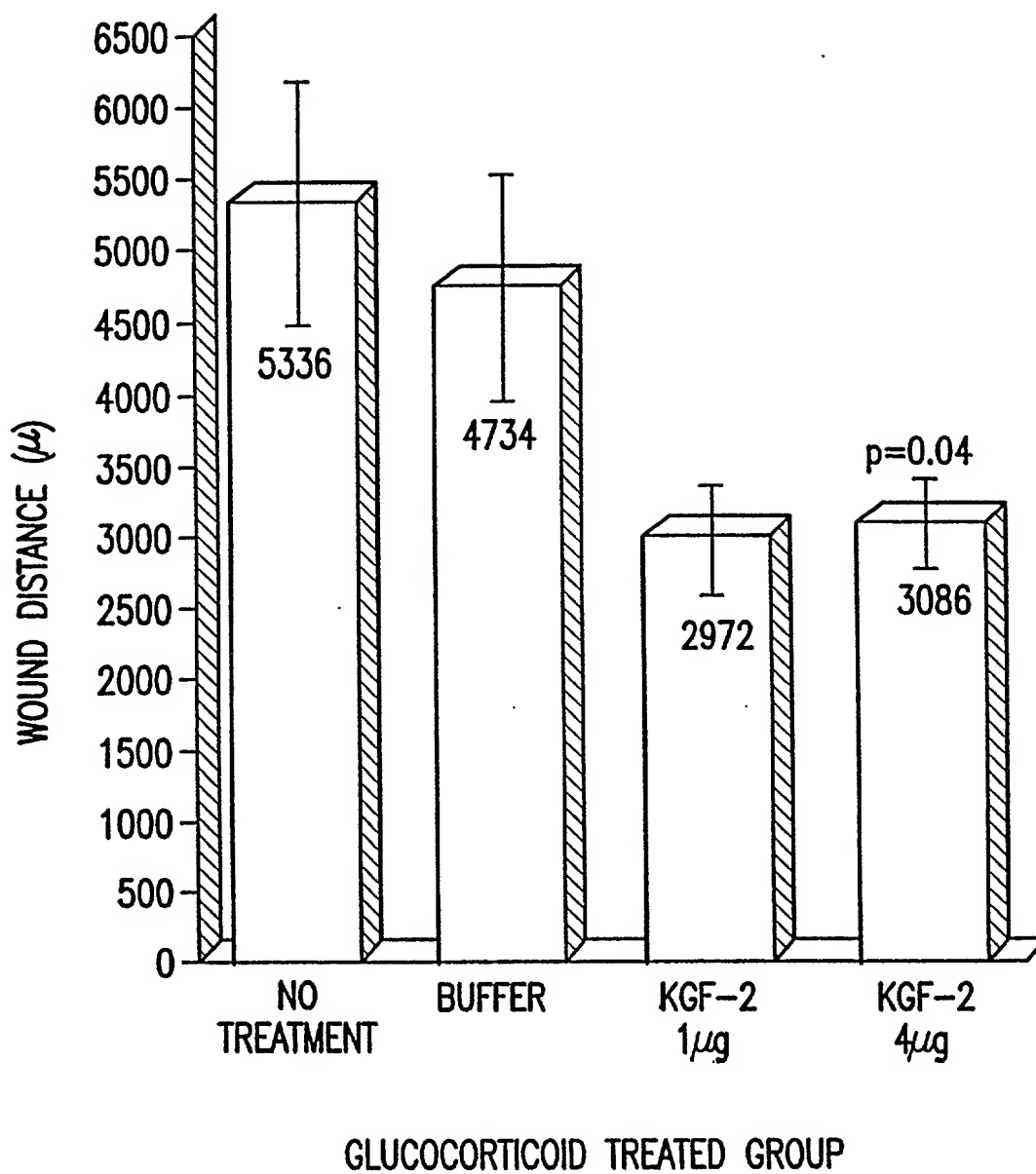


FIG.20

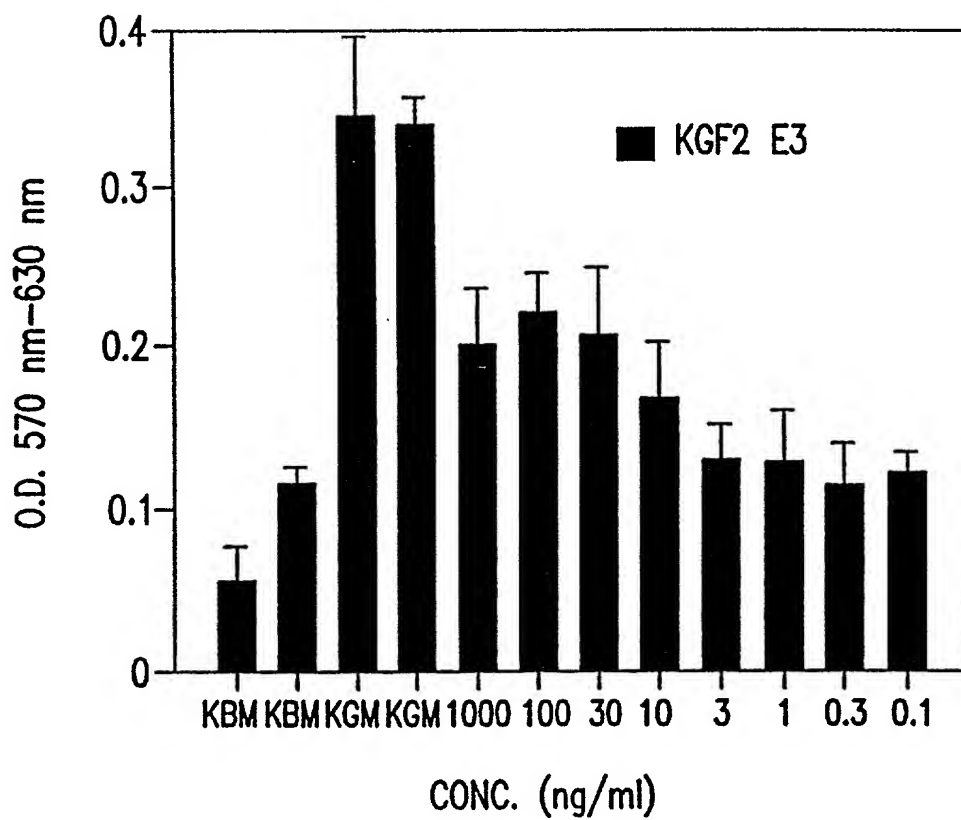


FIG.21A

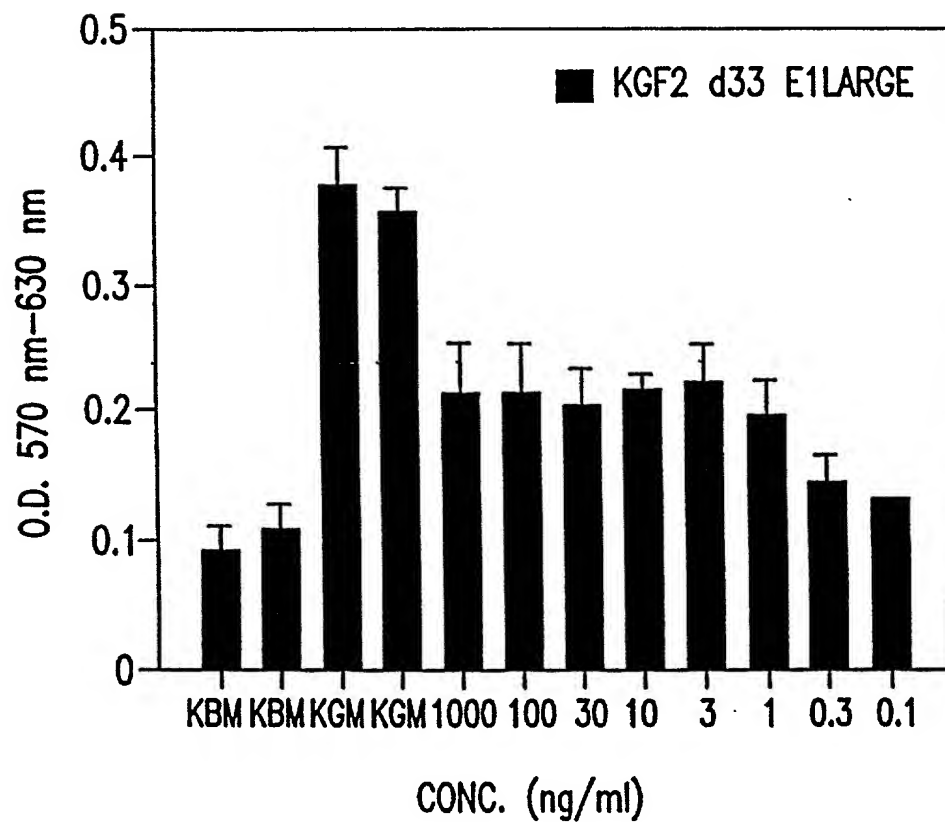


FIG.21B

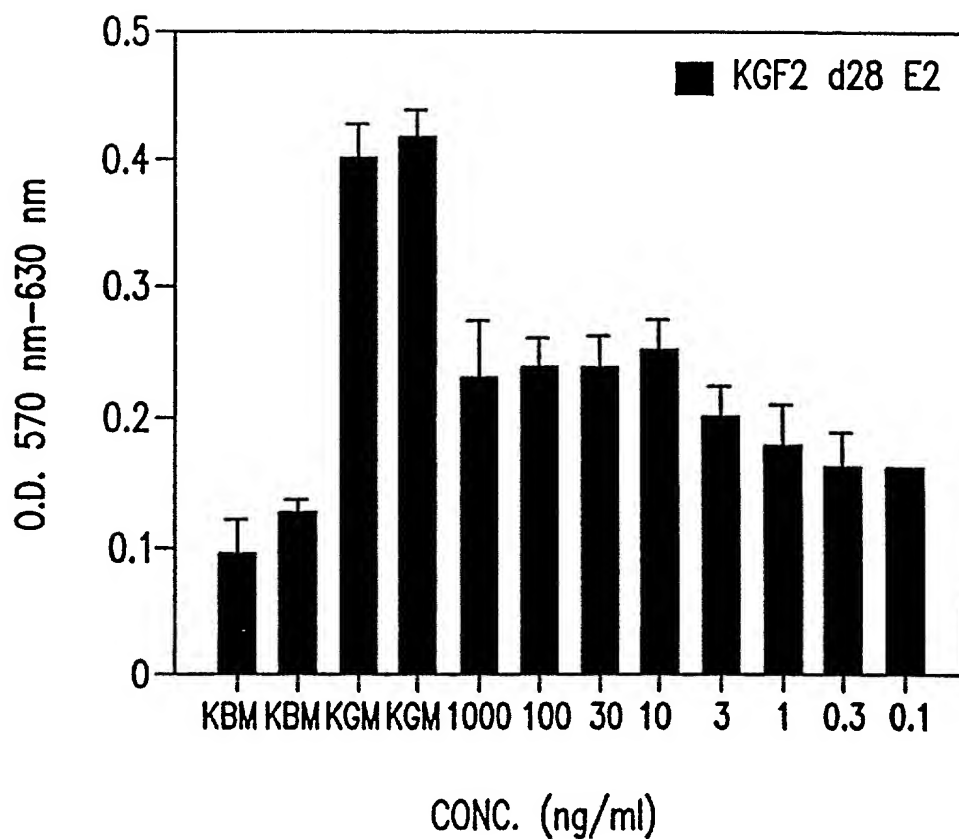


FIG.21C

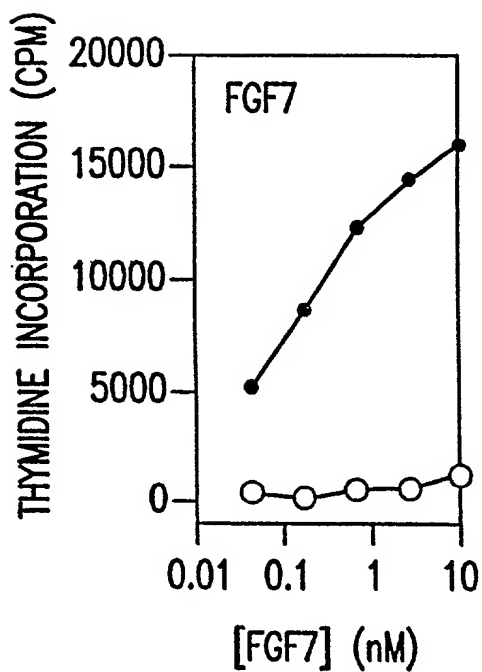


FIG.22A

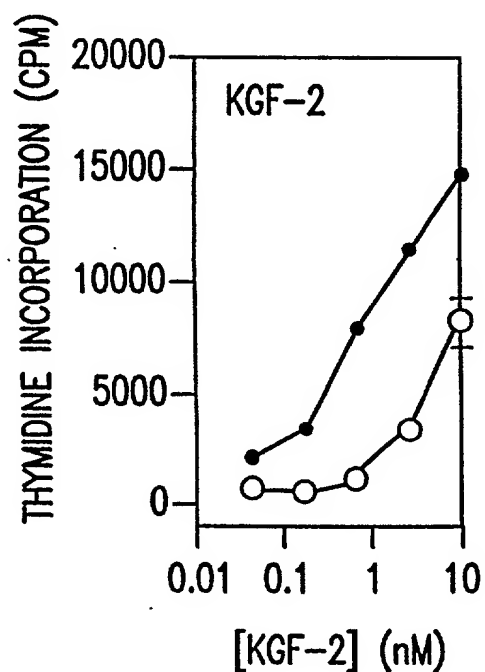


FIG.22A-1

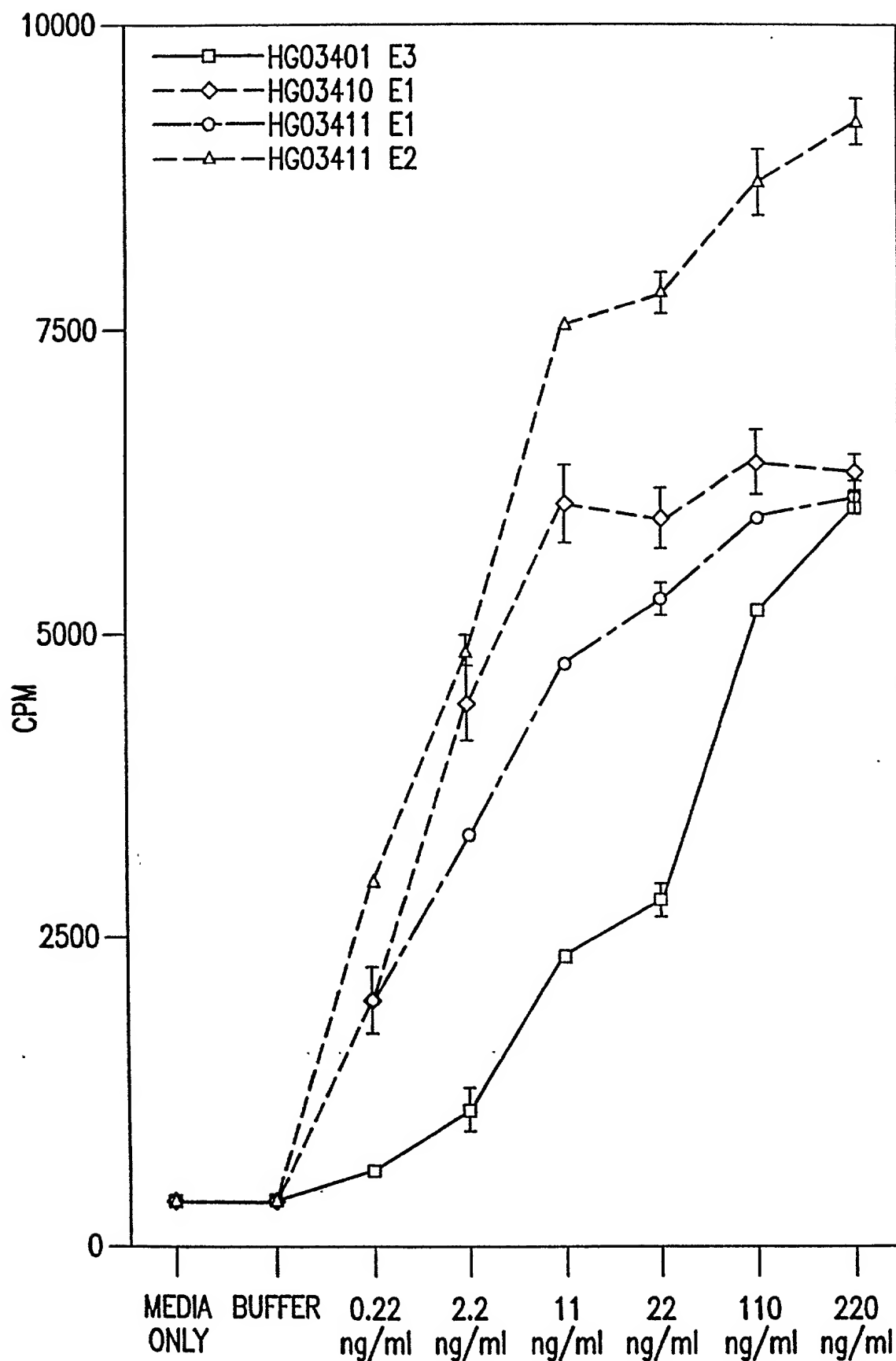


FIG.22B

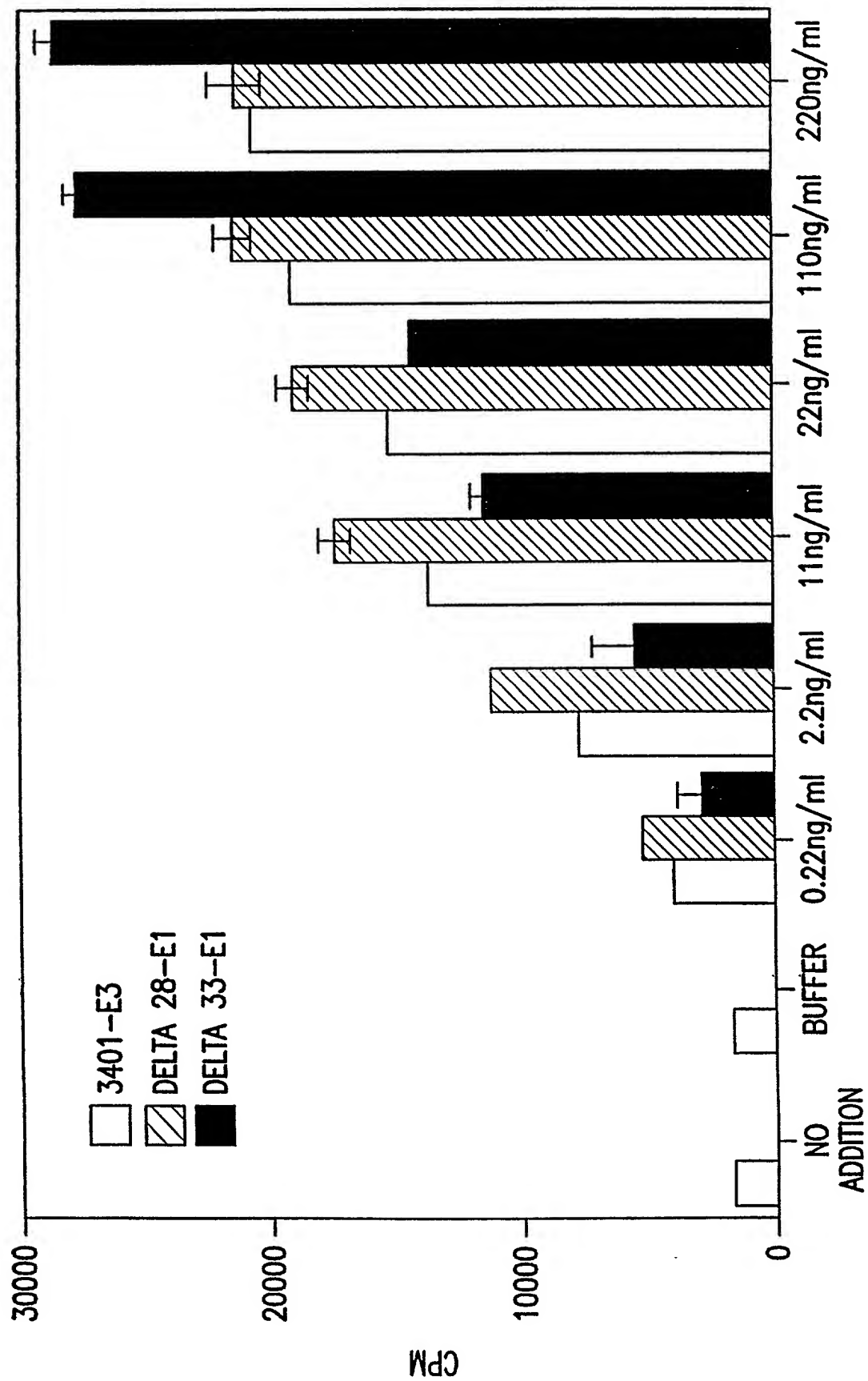


FIG.22C

ATGTGGAATGGATACTGACCCACTGCGCTTCTGCTTTCCCGCACCTGCCGGGTGCTGC 60  
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly Cys Cys  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TGCTGCTGCTTCCTGCTGCTGTTCTGTTCTTCTGTTCCGGTTACCTGCCAGGCTCTG 120  
Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro Val Thr Cys Gln Ala Leu  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCTCTTTCTCTTCCCCG 180  
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ACTTCCGCTGGTCGTCACGTTCTTCTTACAACCACCTGCAGGGTGACGTTCTGTTGGCGT 240  
Thr Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCTGGG 300  
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360  
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC 420  
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480  
Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 540  
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC 600  
Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TTTCTTCCAATGGTGGTACACTCATAG 627  
Phe Leu Pro Met Val Val His Ser \*  
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

FIG.23

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT 60  
 MetThrCysGlnAlaLeuGlyGlnAspMetValSerProGluAlaThrAsnSerSerSer  
 TCCTCTTTCTCTTCCCCGCTCTCCGCTGGTCGTCACGTTGTTCTTACAACCACCTGCAG 120  
 SerSerPheSerSerProSerSerAlaGlyArgHisValArgSerTyrAsnHisLeuGln  
 GGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA 180  
 GlyAspValArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysIleGluLys  
 AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA 240  
 AsnGlyLysValSerGlyThrLysLysGluAsnCysProTyrSerIleLeuGluIleThr  
 TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG 300  
 SerValGluIleGlyValValAlaValLysAlaIleAsnSerAsnTyrTyrLeuAlaMet  
 AACAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAG 360  
 AsnLysLysGlyLysLeuTyrGlySerLysGluPheAsnAsnAspCysLysLeuLysGlu  
 AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420  
 ArgIleGluGluAsnGlyTyrAsnThrTyrAlaSerPheAsnTrpGlnHisAsnGlyArg  
 CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480  
 GlnMetTyrValAlaLeuAsnGlyLysGlyAlaProArgArgGlyGlnLysThrArgArg  
 AAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525  
 LysAsnThrSerAlaHisPheLeuProMetValValHisSer \*

FIG.24A

ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA  
 TACTGAACGGTCCGTGACCCAGTTCTGTACCAAAGGGCCTTOGATGGTTGTCGAGGTGAGATCGAAGT  
 M T C Q A L G Q D M V S P E A T N S S S S S F  
 GCAGCCCATCTAGCGCAGGTGCTCAGTTGCTCTTACAACCACTTACAGGGTGATGTTGCTTGGCGCAA  
 CGTCGGGTAGATCGGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGGTT  
 S S P S S A G R H V R S Y N H L Q G D V R W R K  
 ACTGTTCACTTTACCAAGTACTTCTGAAAATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG  
 TGACAAGTCGAAATGGTTCATGAAGGACTTTTAGCTTTTTTGGCATTTCAAAGACCCTGGTCTTCTCTC  
 L F S F T K Y F L K I E K N G K V S G T K K E  
 AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACA  
 TTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTAGCCTCAACAACGGCAGTTTCGGTAATTGT  
 N C P Y S I L E I T S V E I G V V A V K A I N  
 GCAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAAGAATTAAACAATGACTGTAA  
 CGTTGATAATGAATCGGTACTTGTCTTCCCTTTGAGATACCGAGTTTCTTAAATTGTTACTGACATT  
 S N Y Y L A M N K K G K L Y G S K E F N N D C K  
 GCTGAAGGAGAGGATAGAGGAAAATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG  
 CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCTCC  
 L K E R I E E N G Y N T Y A S F N W Q H N G R  
 CAAATGTATGTGGCATTGAATGAAAAGGAGCTCAAGGAGAGGACAGAAAACGGAAGGAAAAACACCT  
 GTTACATACACCGTAACCTTACCTTTTCTCGAGGTTCTCTCTCTTGTGCTTCTTTTGTGGA  
 Q M Y V A L N G K G A P R R G Q K T R R K N T  
 CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG  
 GACGAGTGAAGAAGGTTACCACCATGTGAGTATC  
 S A H F L P M V V H S

FIG.24B



2040 2500 103513 010402

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCACGTTTCGTTCTTACAACCAC  
CTGCAGGGTGACGTTTCGTTGGCGTAAACTGTTCTTTTACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTAAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSAGRHVRSYNHLQGDVWRKLFSTKYFLKIE  
KNGKVSQTKKENCYPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKL  
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.25

ATGGCTGGTCGTCACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTTCGTTGGCGT  
AAACTGTTCTCTTTTACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT  
GGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAAG  
GGGAAACTCTATGGCTCAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATA  
GAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAA  
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG  
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVWRKLFSTKYFLKIEKNGKVSQTKKENCYPYSILEITSVEIGV  
VAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA  
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.26

ATGGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAA  
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATA  
ACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTA  
GCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAG  
CTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAG  
CATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA  
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA  
TAG

MVRWRKLFSTKYFLKIEKNGKVSgtKKENCpysILEITSVEIGVVAVKAINSnyLLAM  
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR  
RKNTSAHFLPMVVHS.

FIG.27

ATGGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCAT  
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCA  
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTTAAC  
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC  
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG  
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA  
ATGGTGGTACACTCATAG

MEKNGKVSgtKKENCpysILEITSVEIGVVAVKAINSnyLLAMNKKGKLYGSKEFNND  
KLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH  
S.

FIG.28

ATGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT  
TGCCGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC  
TCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA  
AATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTA  
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA  
ACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPSYLEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGY  
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

## FIG.29

ATGGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAACT  
CTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA  
ATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT  
GTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA  
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY  
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

## FIG.30

ATGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG  
GATAGAGGAAAATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA  
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACA  
CGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT  
RRKNTSAHFLPMVVHS.

## FIG.31

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCAC  
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT  
GACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSTKYFLKIE  
KNGKVSGETTKENCPYSILEITSVEIGVVAVKAINSYYLAMNKKGKLYGSKEFNNDCKL  
K

FIG.32

ATGGCTGGTCGTCACGTTGTTCTTACAACCACCTGCAGGGTGACGTTGTTGGCGT  
AACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT  
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG  
GGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSTKYFLKIEKNGKVSGETTKENCPYSILEITSVEIGV  
VAVKAINSYYLAMNKKGKLYGSKEFNNDCKLK

FIG.33

C-37 To Ser

ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCAC  
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTAAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

FIG.34

C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCAC  
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTAAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

FIG.35

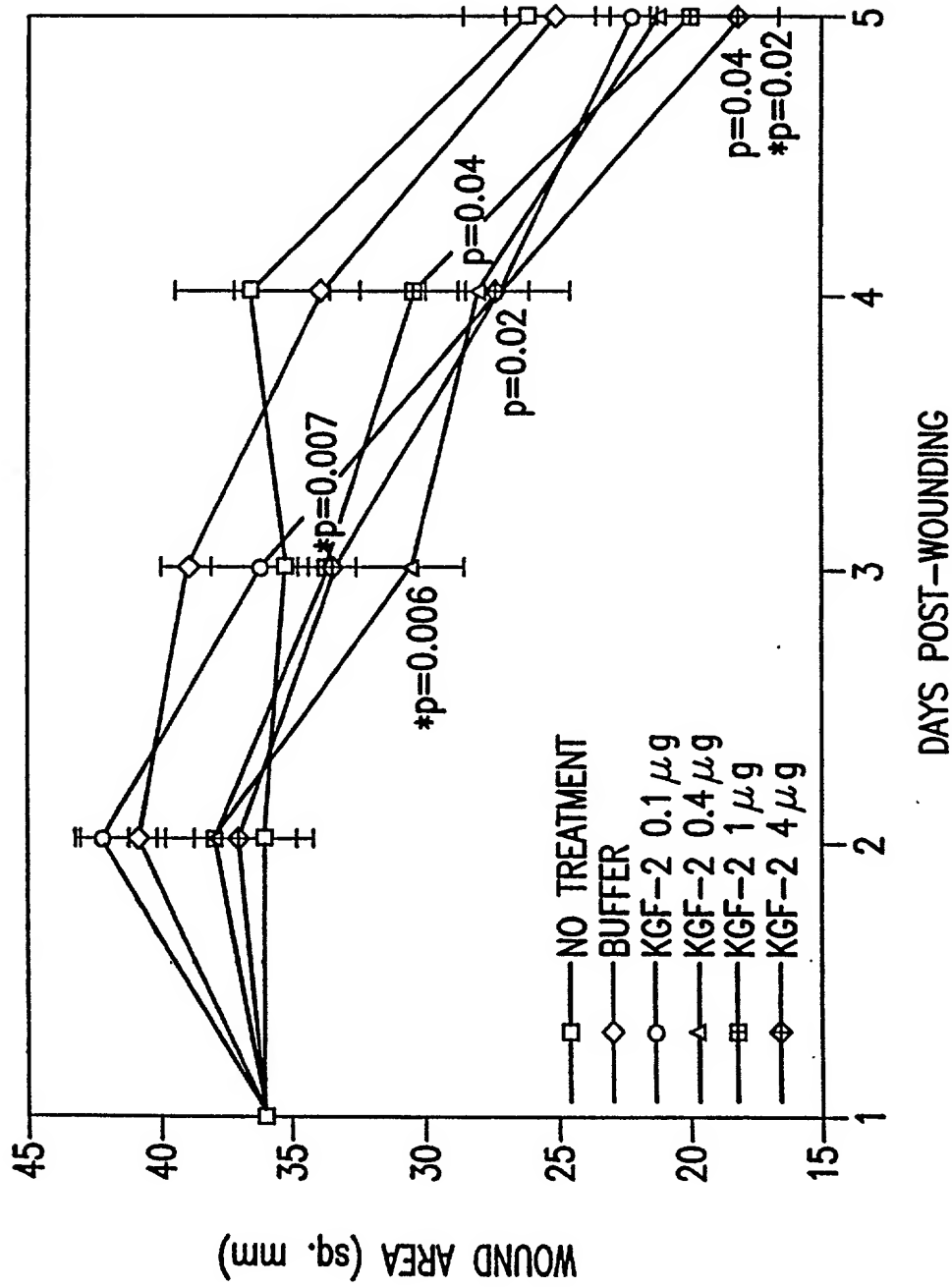


FIG.36

EFFECT OF KGF-2 Δ33 ON NORMAL WOUND HEALING RAT MODEL

TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. (μm)	BrdU SCORE
NO TREATMENT	25.9±2.5	58.8±3.7	6.8±0.2	1142±141	3.8±0.4
BUFFER	25.1±1.7	60.2±2.6	6.4±0.2	923±61	5.0±0.4
KGF-2/Δ33 (0.1μg)	22.0±0.9	65±1.4	6.8±0.2	1275±148	4.6±0.7
KGF-2/Δ33 (0.4 μg)	21.1±1.4	68.4±2.4	8.0±0.5 p=0.0445*	1310±182	4.2±0.7
KGF-2/Δ33 (1.0 μg)	19.9±1.5	66.2±2.1	8.4±0.4 p=0.0159* p=0.0053†	1389±115 p=0.0074†	3.3±0.25 p=0.0217†
KGF-2/Δ33 (4.0μg)	18.1±1.6 p=0.0398* p=0.0200†	71.2±2.6 p=0.0367* p=0.0217†	8.5±0.3 p=0.0047* p=0.0445†	1220±89 p=0.0254†	5.3±0.9

FIG.37

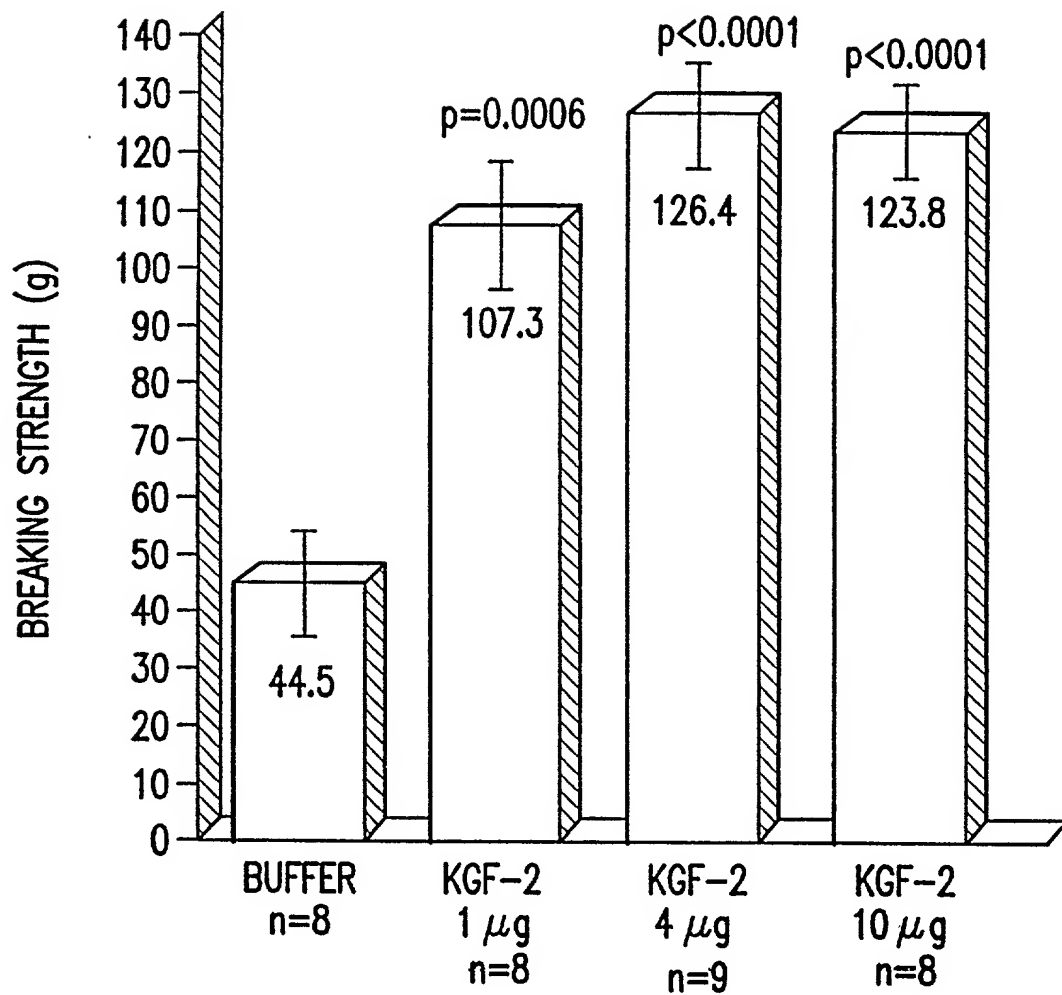


FIG.38



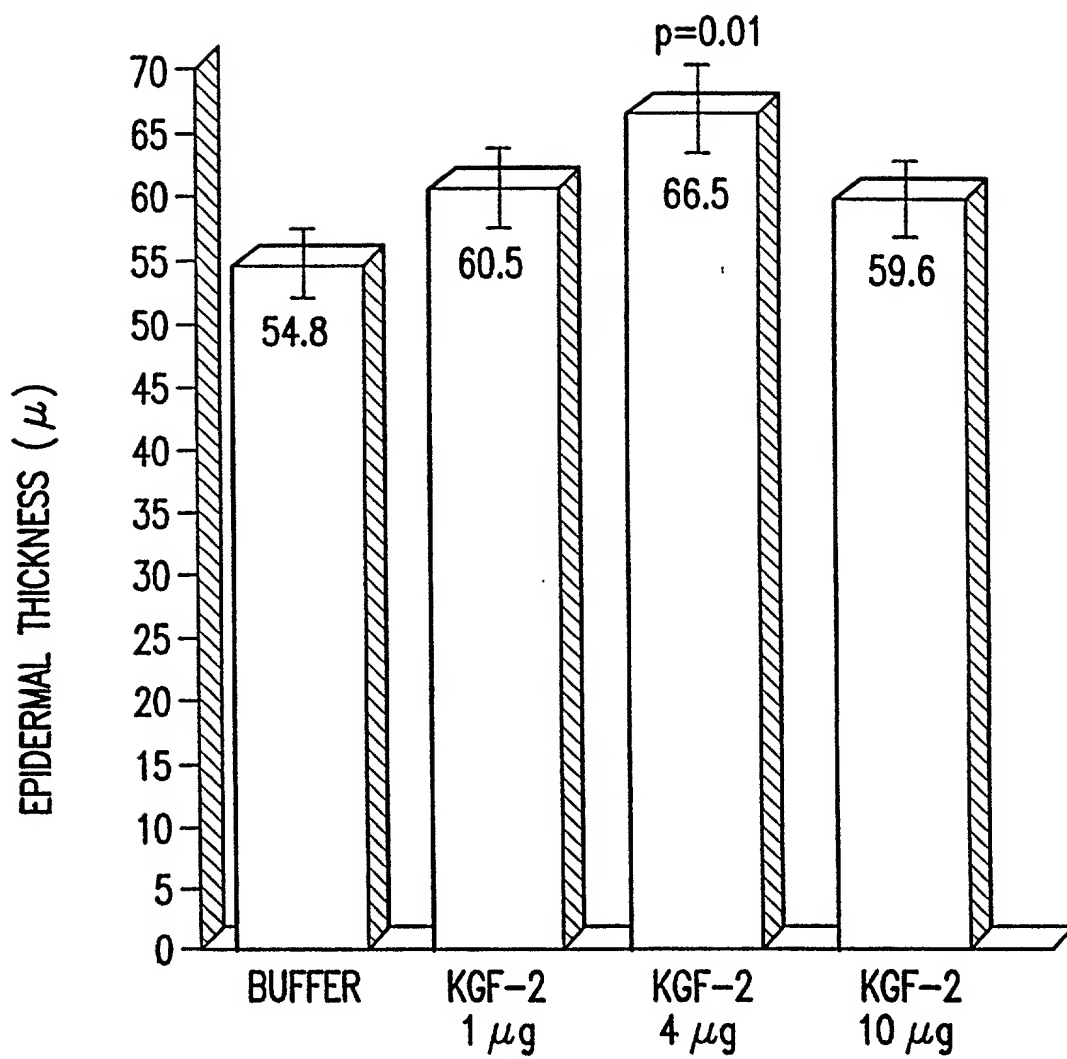


FIG.39

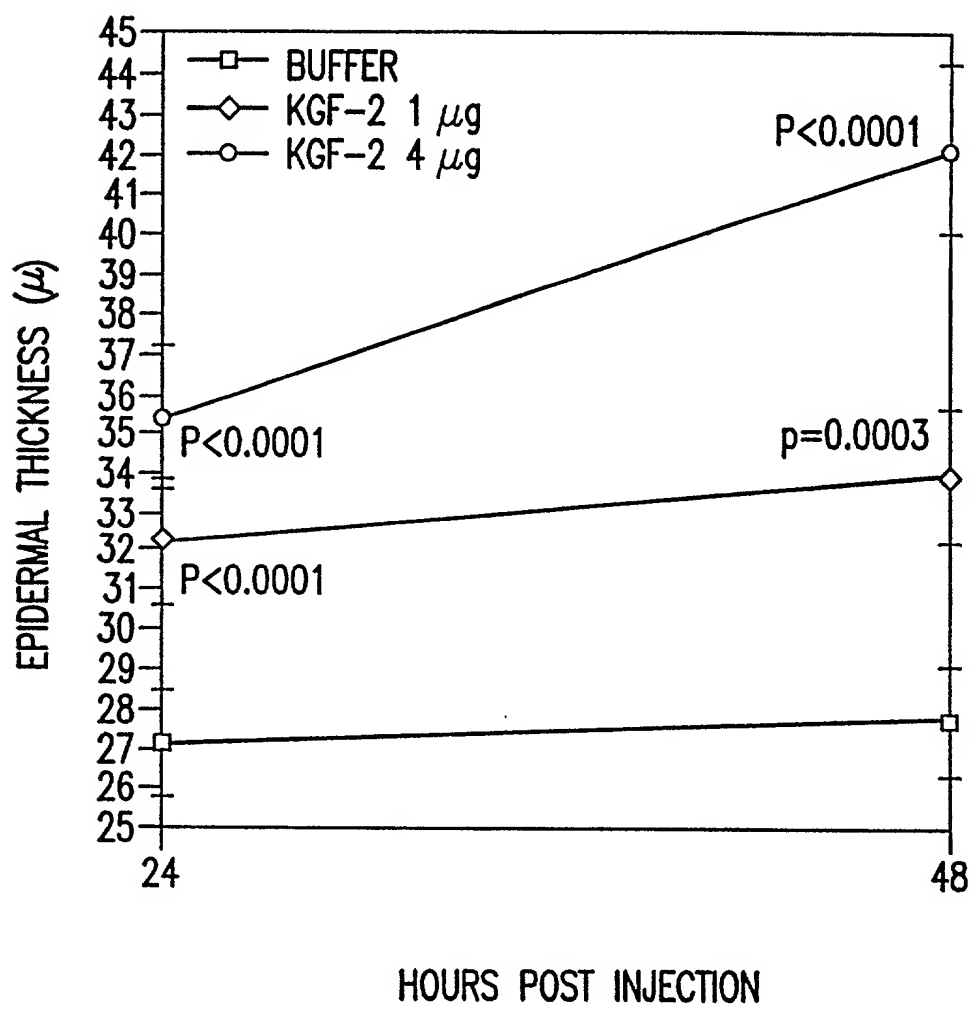


FIG.40

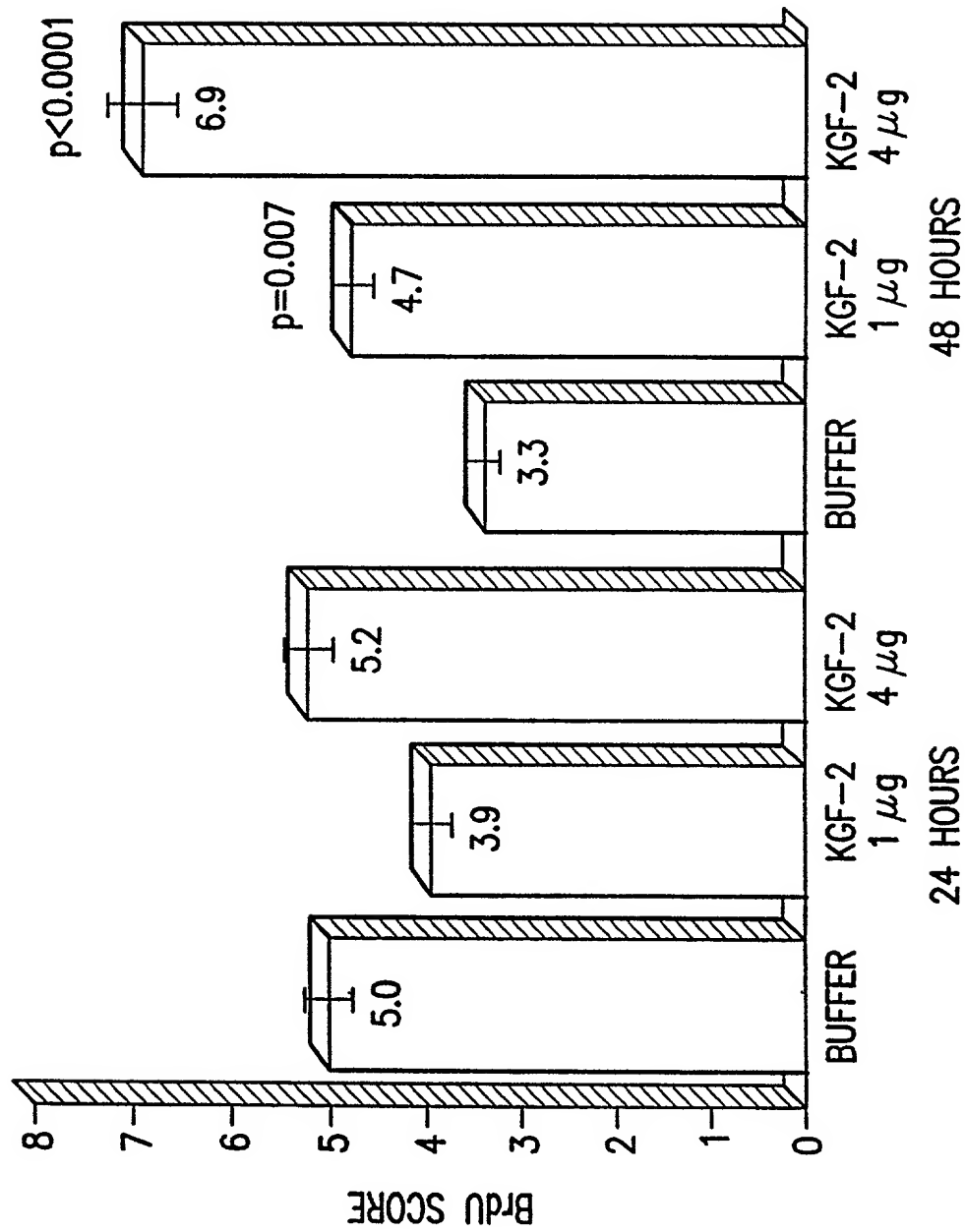


FIG.41

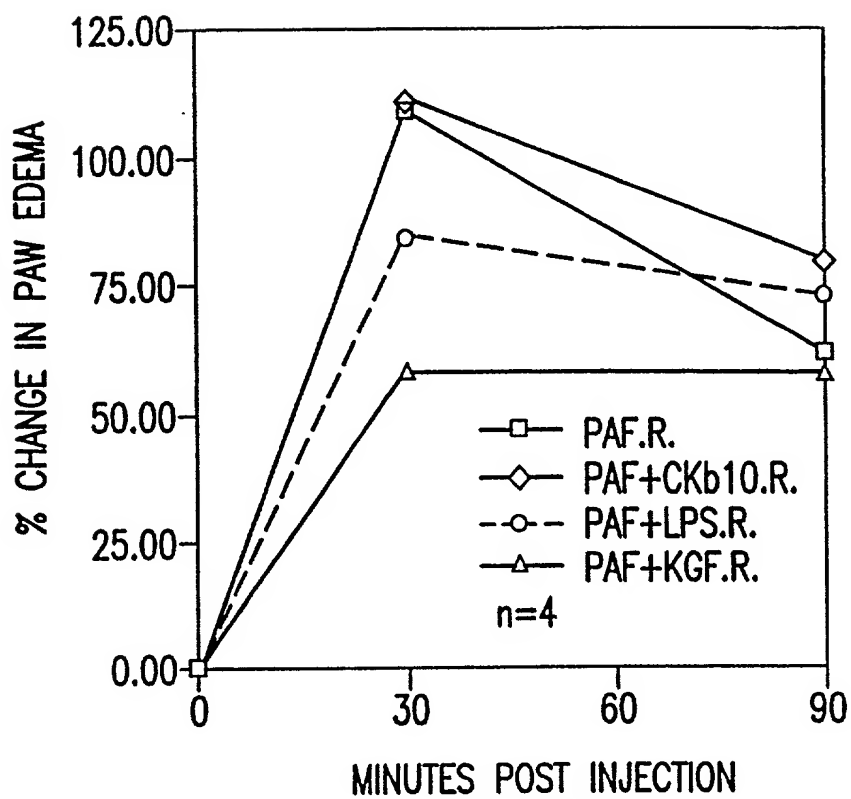


FIG.42A

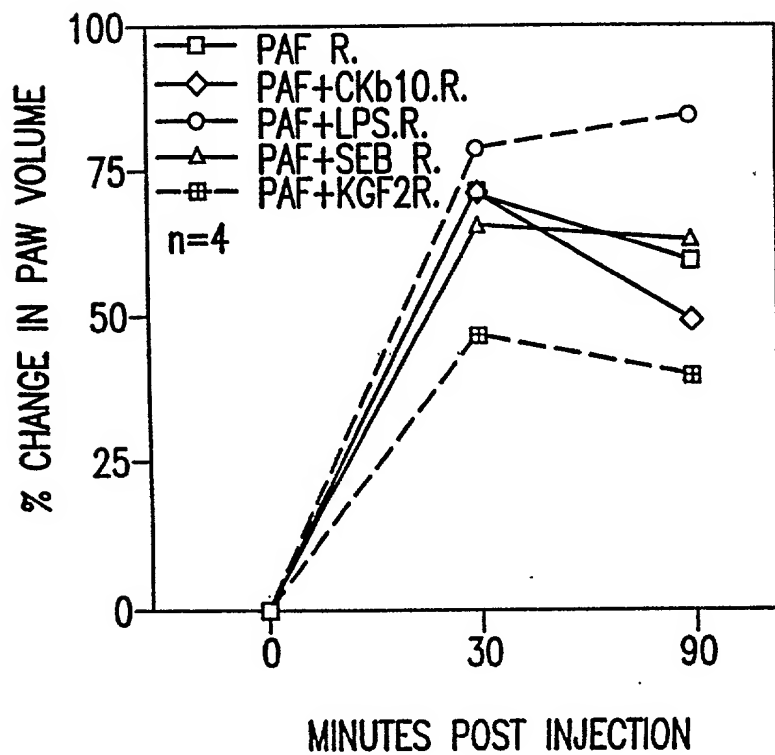


FIG.42B

# EFFECT OF KGF-2 $\Delta 33$ ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

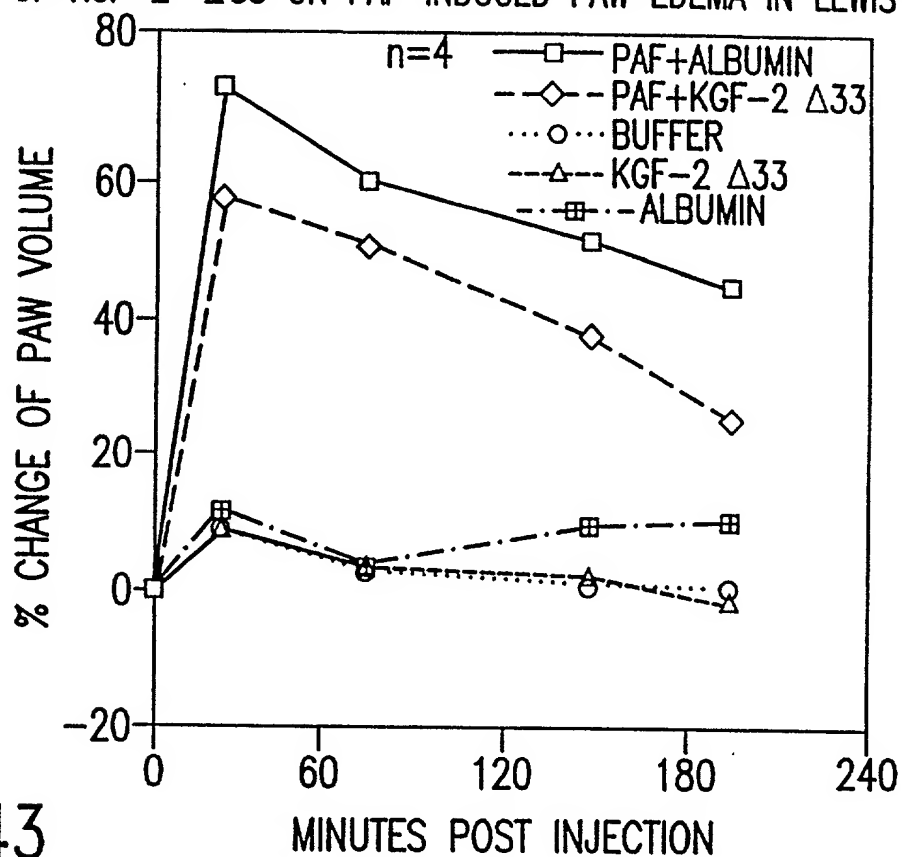


FIG.43

# EFFECT OF KGF-2 $\Delta 33$ ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

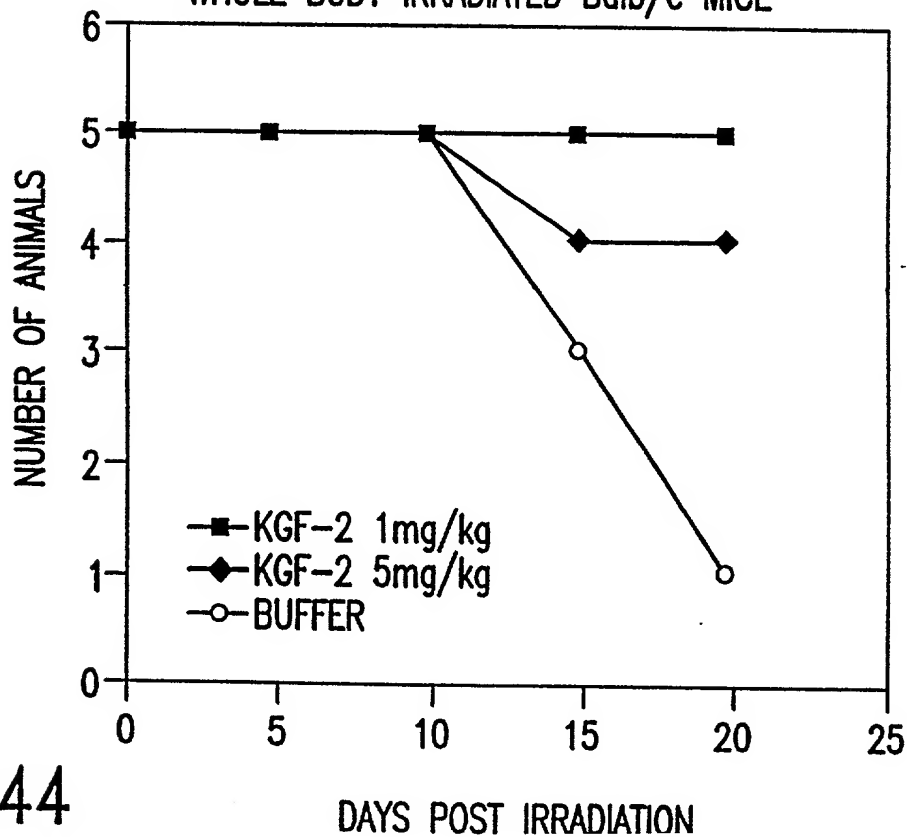


FIG.44

# EFFECT OF KGF-2 $\Delta 33$ ON BODY WEIGHT OF IRRADIATED MICE

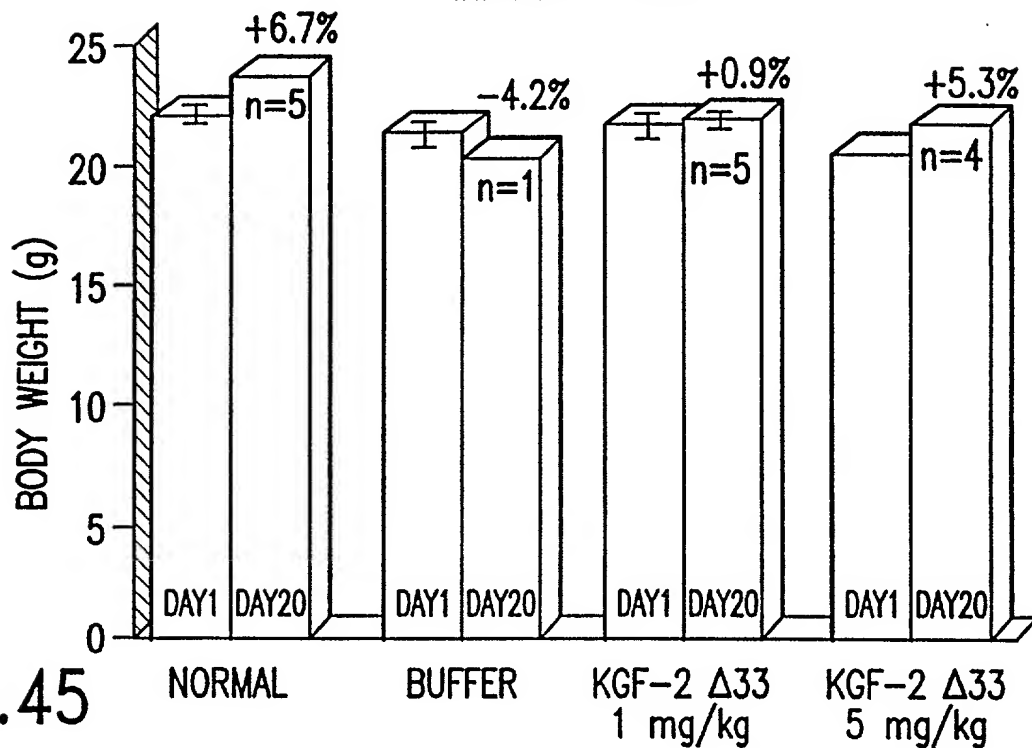
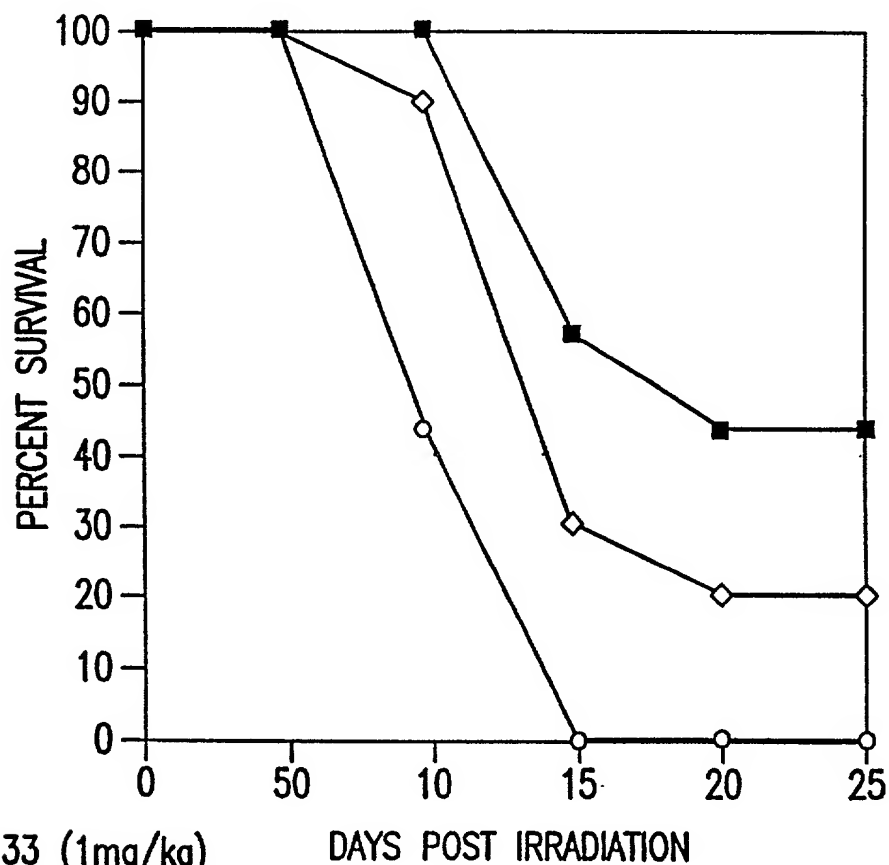


FIG.45



◇ KGF-2  $\Delta 33$  (1mg/kg)  
 ■ KGF-2  $\Delta 33$  (5mg/kg)  
 ○ BUFFER

DAYS POST IRRADIATION

FIG. 46

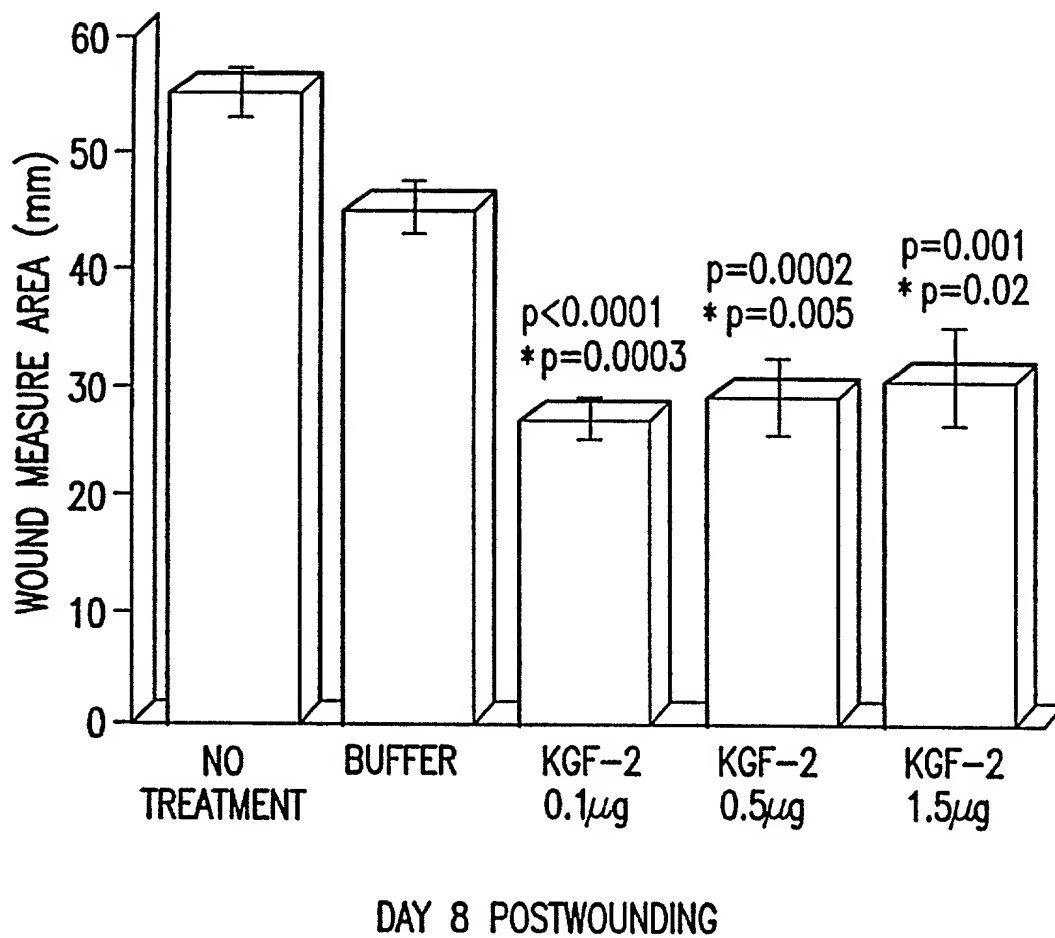


FIG.47

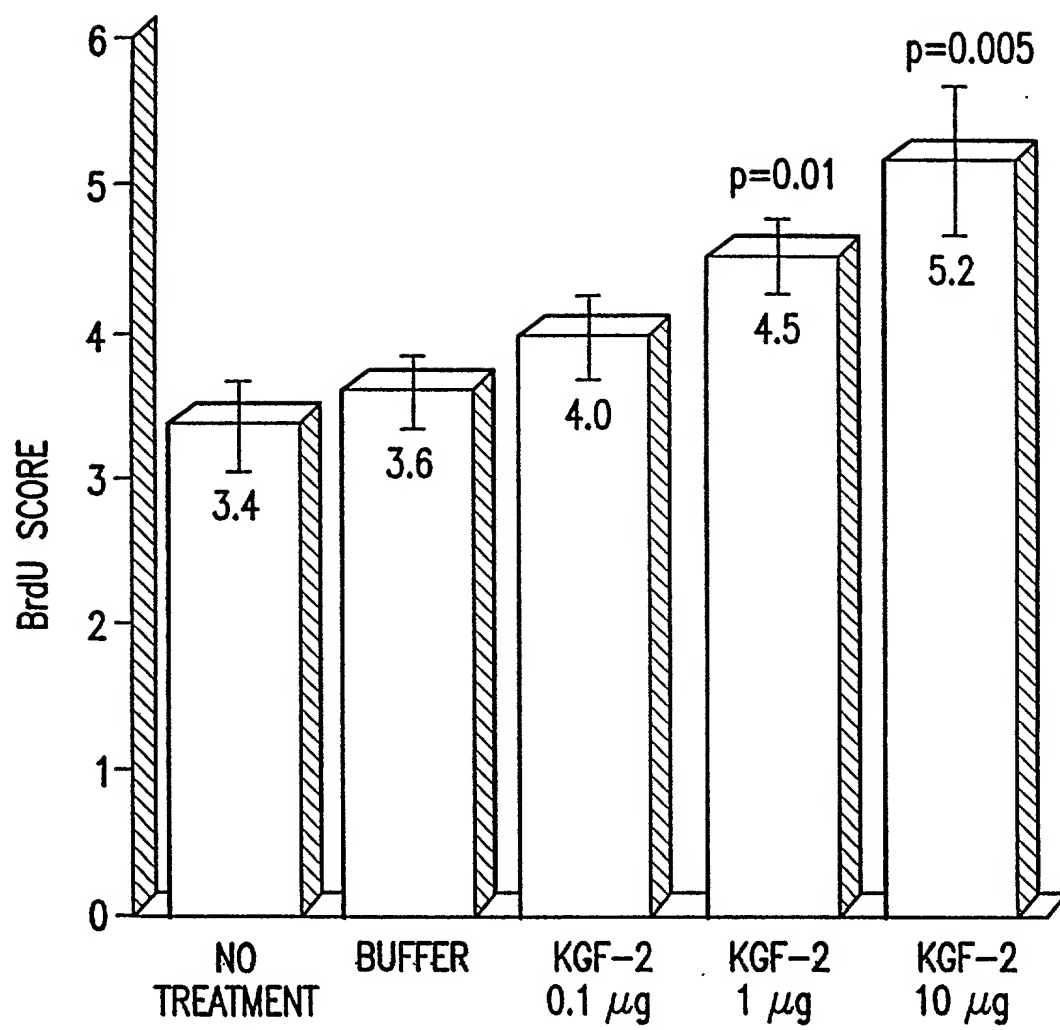


FIG.48



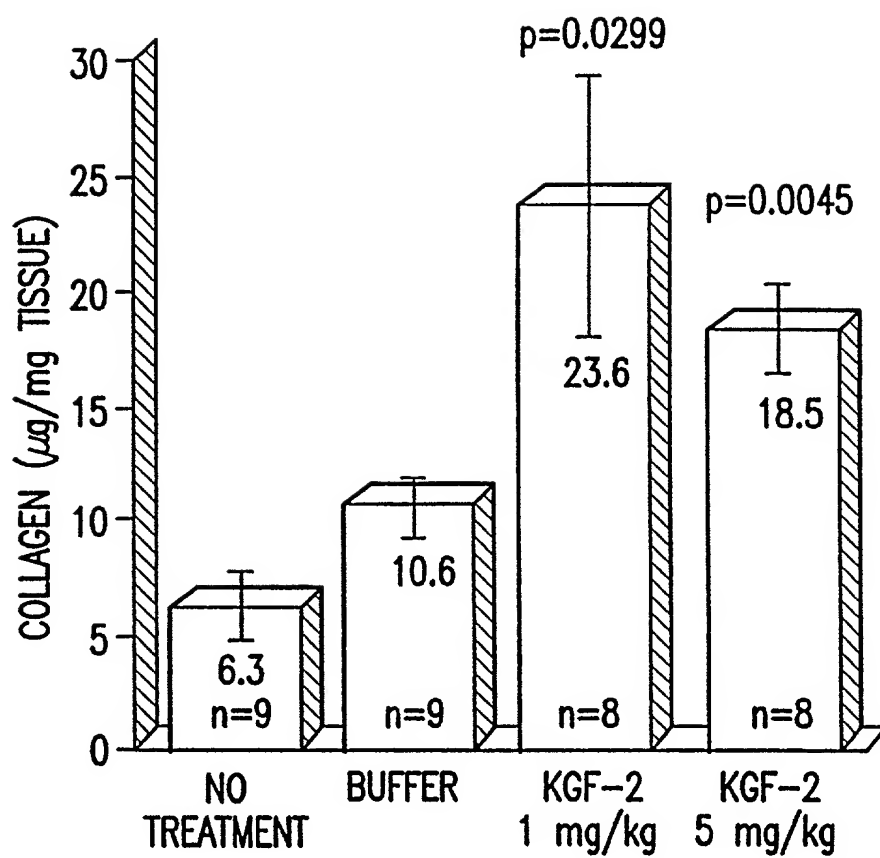


FIG.49

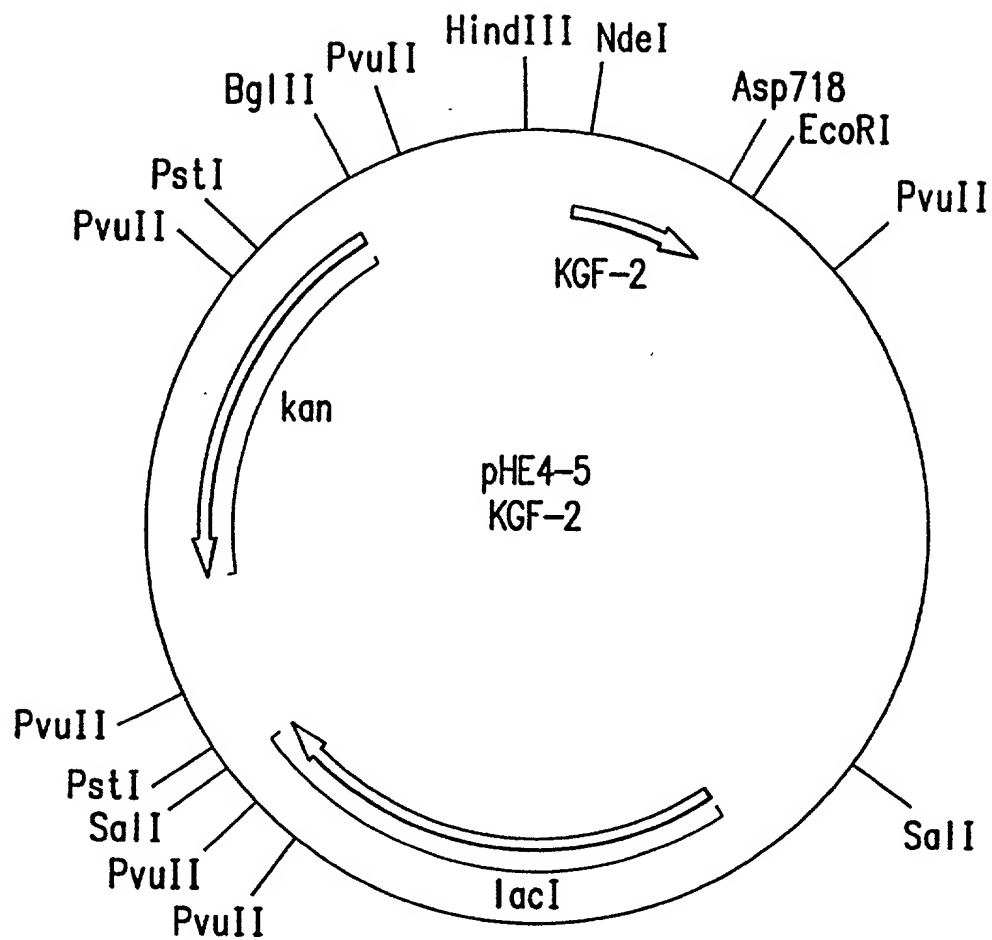


FIG. 50

1      AAGCTTAAAAAACTGCAAAAATAGT <sup>-35</sup> T T G A C T <sup>Operator 1</sup> (TGTGAGCGGATAACAAT)

50      <sup>-10</sup> (TAAGAT)GTACCCAATTGTGAGCGGATAACAAT <sup>Operator 2</sup> TTCACACATTAA

94      <sup>S/D</sup> (AGAGGAG)AAATTA CATATG

FIG. 51

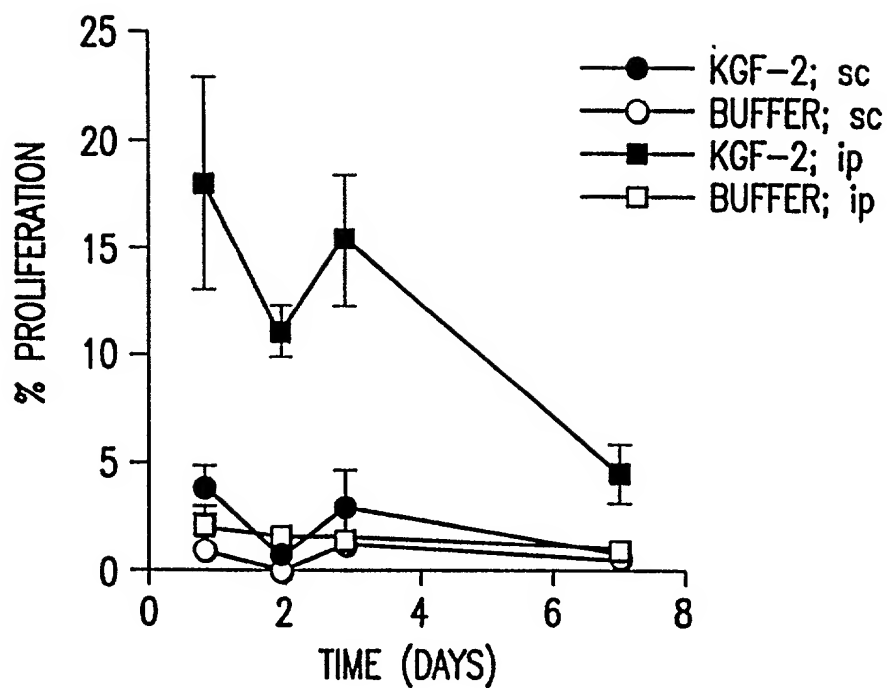


FIG. 52

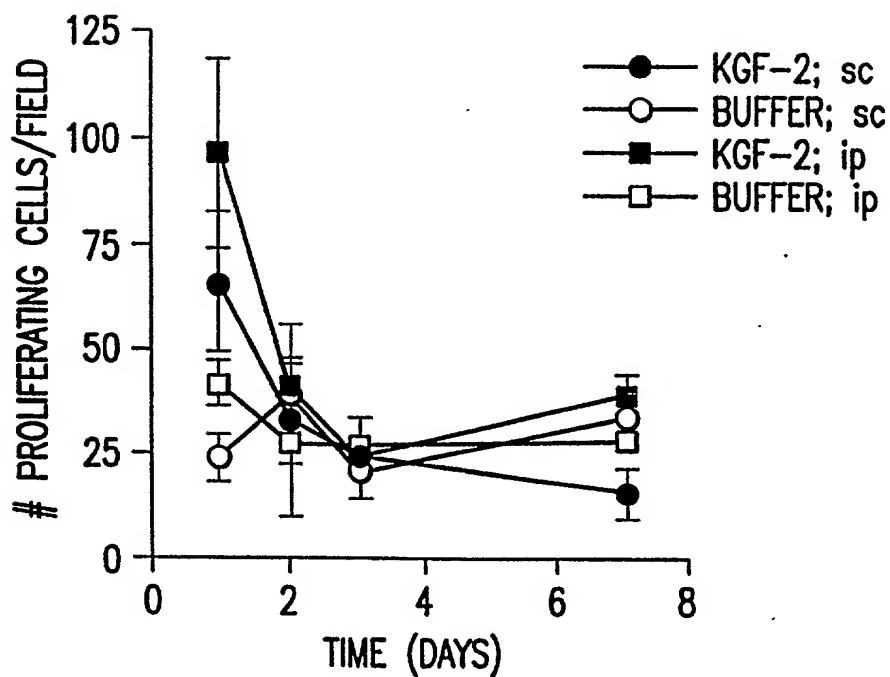


FIG. 53

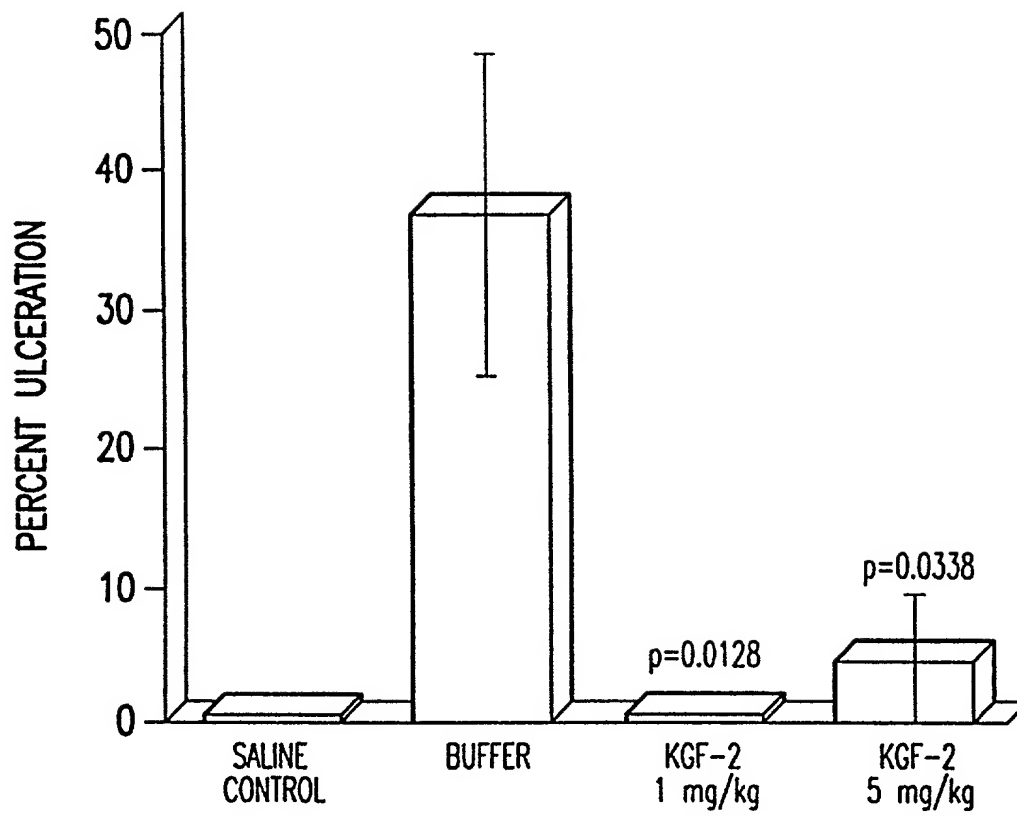


FIG. 54

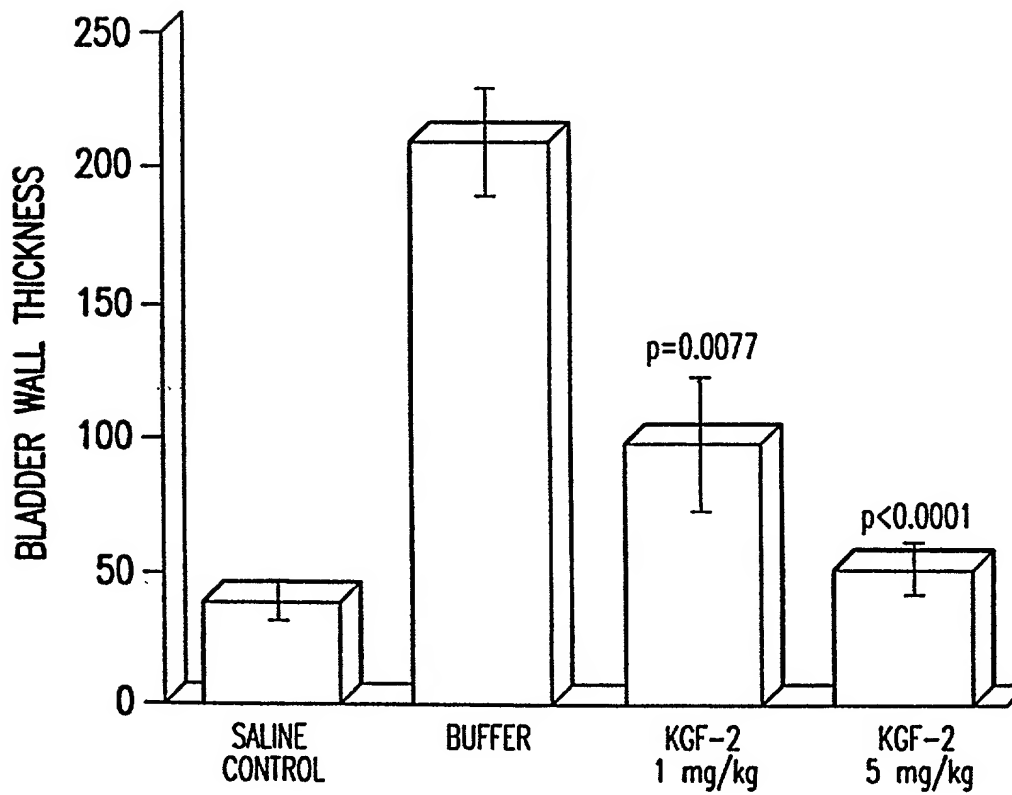


FIG. 55

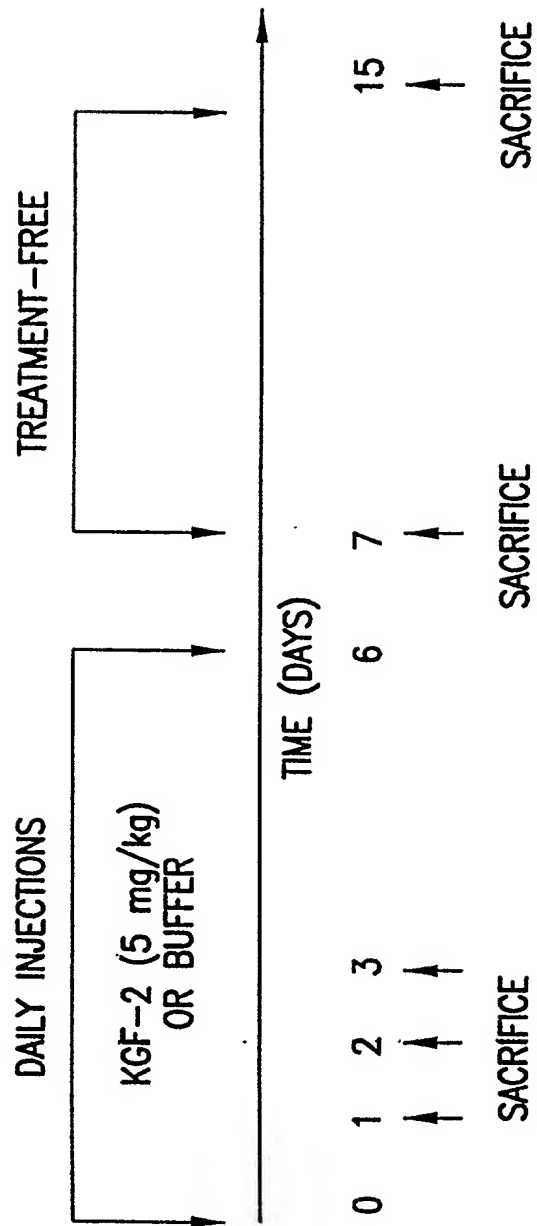


FIG. 56

# PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

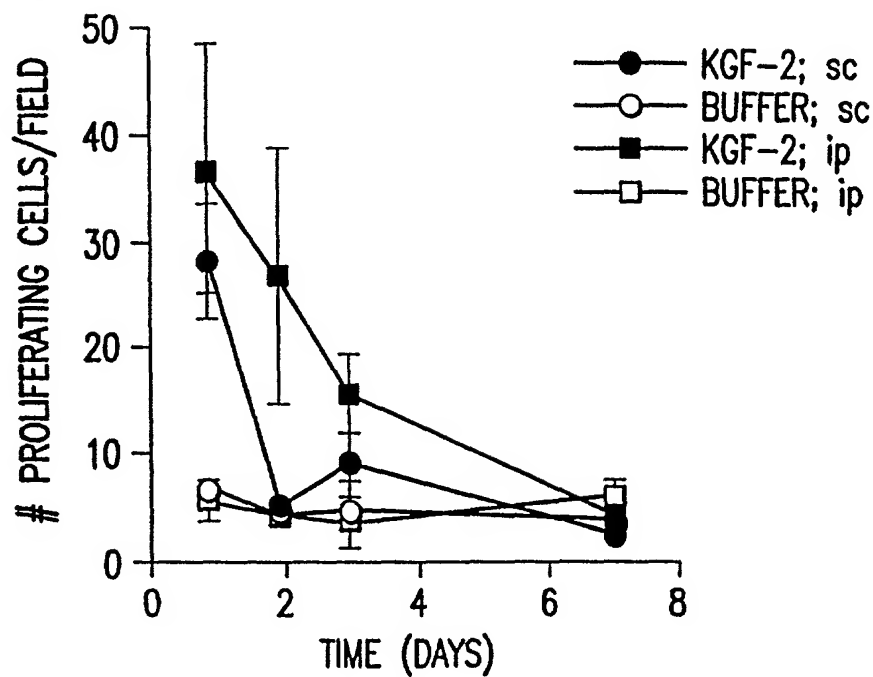


FIG. 57

# PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

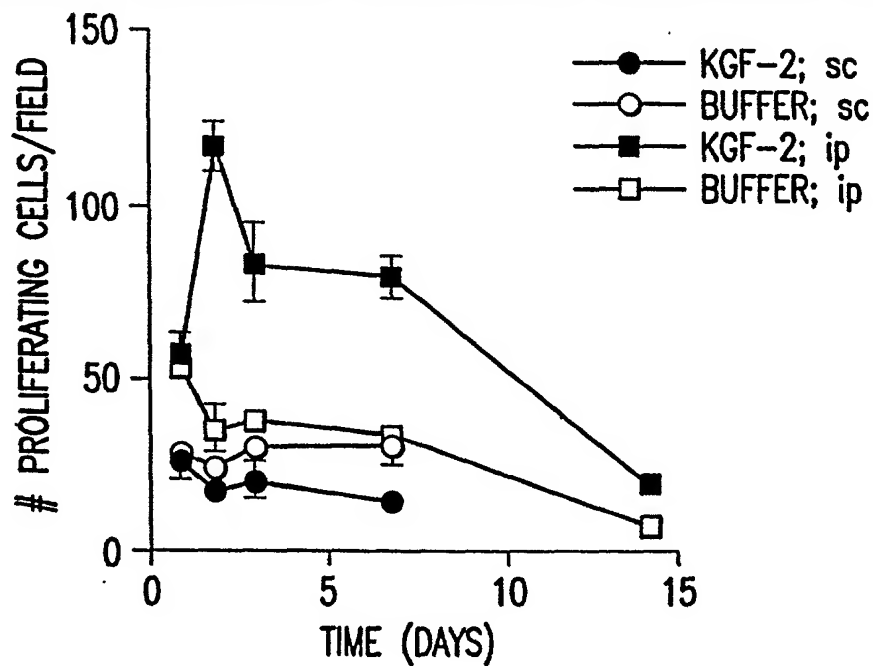


FIG. 58

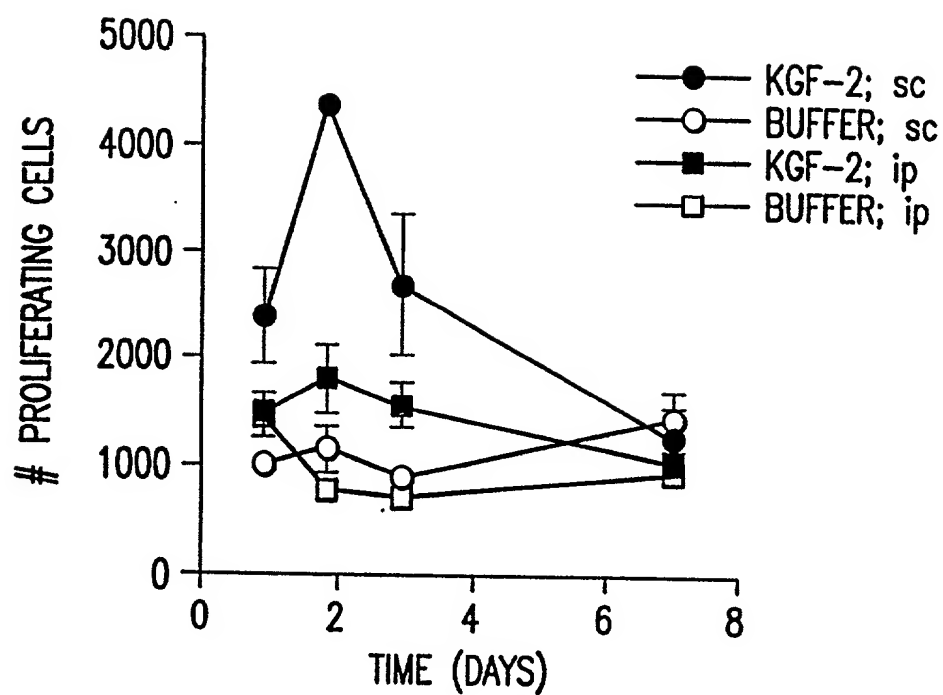


FIG. 59

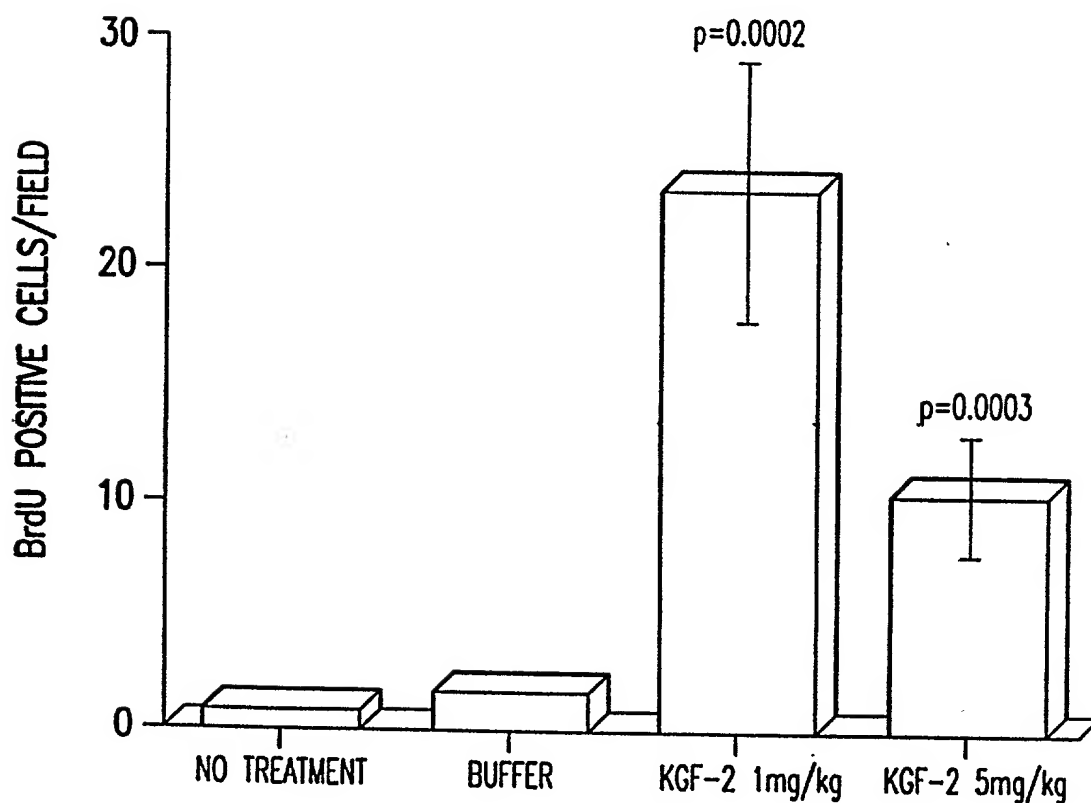


FIG. 60